

A77N: Ed Hart.

127401

Access DB# \_\_\_\_\_

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 7/15/04  
 Art Unit: 1636 Phone Number: 272-0777 Serial Number: 09/845064  
 Mail Box and Bldg. Room Location: 2A89/REN Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Clean syn. vector. plasmids, 76 plants...

Inventors (please provide full names): Gruber, V. et al.

Earliest Priority Filing Date: 9/3/1999

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please search SEQ ID NO: 10 both interference & commercial database.*

## STAFF USE ONLY

Searcher: \_\_\_\_\_

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date searched: 7/16/04Date indexed: 7/21/04

Searcher Prep &amp; Review Time: \_\_\_\_\_

Clerical Prep Time: \_\_\_\_\_

Indexing Time: \_\_\_\_\_

## Type of Search

NA Sequence (#) 1

AA Sequence (#) \_\_\_\_\_

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other: \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel Orbit \_\_\_\_\_

OCLink \_\_\_\_\_

Lexis Nexis \_\_\_\_\_

Sequence Systems Q3H

WWW Internet \_\_\_\_\_

Other vendors: \_\_\_\_\_

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# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 127401**

**TO: Celine Qian**  
**Location: REM-2A89/2C70**  
**Art Unit: 1636**  
**Wednesday, July 21, 2004**

**Case Serial Number: 09/845064**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**REM-1A55**  
**Phone: 571-272-2512**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 06:57:16 ; Search time 18105 Seconds  
(without alignments)  
11503.081 Million cell updates/sec

Title: US-09-845-064-10

Perfect score: 4805

Sequence: 1 ccgggtggttcctcgcce.....gagcgctttggagcgctca 4805

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

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40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4805	100.0	4805	6	AX093005 Sequence
2	4590.8	95.5	7943	6	AX093010 Sequence
3	4549	94.7	10003	6	AX093016 Sequence
4	4531.4	94.3	5614	6	AX093011 Sequence
5	4531.4	94.3	5971	6	AX092998 Sequence
6	4531.4	94.3	6016	6	AX092999 Sequence
7	4531.4	94.3	6016	6	AX093001 Sequence
8	4531.4	94.3	6017	6	AX093000 Sequence
9	4531.4	94.3	6017	6	AX093002 Sequence
10	4531.4	94.3	6767	6	AX093003 Sequence
11	4531.4	94.3	6767	6	AX093004 Sequence
12	4531.4	94.3	6865	6	AX093008 Sequence
13	4531.4	94.3	7503	6	AX093012 Sequence
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15	4531.4	94.3	8289	6	AX093050 Sequence
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17	4531.4	94.3	8987	6	AX093017 Sequence
18	4531.4	94.3	9143	6	AX093007 Sequence
19	4531.4	94.3	9285	6	AX093047 Sequence
20	4531.4	94.3	9390	6	AX093015 Sequence
21	4528.2	94.2	8654	6	AX093006 Sequence
22	4528.2	94.2	9390	6	AX093013 Sequence
23	4512	93.9	9688	6	AX093045 Sequence
24	4070	84.7	4098	6	AX092997 Sequence
25	2880	59.9	3508	6	AX092996 Sequence
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42	2536.2	52.8	14446	6	AX275255 Sequence
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ALIGNMENTS

RESULT 1	AX093005	4805 bp	DNA	linear	PAT 30-MAR-2001
LOCUS	Sequence 10 from Patent WO0118192.				
DEFINITION	AX093005				
ACCESSION	AX093005				
VERSION	AX093005.1	GI:13509479			
SOURCE	.				
KEYWORDS	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1				
AUTHORS	Gruber, V. and Comeau, D.				
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them				
JOURNAL	Patent: WO 0118192-A 10 15-MAR-2001;				

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		/note="NPT III gene coding for neomycin phosphotransferase and kanamycin resistance"
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terminator	4272..4559	
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		/note="MCS multiple cloning site"
misc_feature	4625..4798	
		/note="T-DNA right border"
ORIGIN		
Query Match 100.0%; Score 4805; DB 6; Length 4805;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 4805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	CCGGCTGGTGGCTCCCTCGCGCTGGCTGGCGCGCTGTATGGCCCTGCAAACCGCCAG 60
Db	1	CCGGCTGGTGGCTCCCTCGCGCTGGCTGGCGCGCTGTATGGCCCTGCAAACCGCCAG 60
Qy	61	AAAGCCGTGAGCCGTGTCGAGACACCGCGCCGCGGTGGTGGTACCTCCGCG 120
Db	61	AAAGCCGTGAGCCGTGTCGAGACACCGCGCCGCGGTGGTGGTACCTCCGCG 120
Qy	121	AAACTTGGCCCTCAGTACAGATGAGGGCGGACGTTGACACTTGGAGGCGCCACTCAC 180
Db	121	AAACTTGGCCCTCAGTACAGATGAGGGCGGACGTTGACACTTGGAGGCGCCACTCAC 180
Qy	181	CCGCGCGGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGTGGAGTGGC 240
Db	181	CCGCGCGGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGTGGAGTGGC 240
Qy	241	CAGCTCGAAATCGGCGAAACCCCTGATTTTACGCGAGTTTCCACAGATGATGGGA 300
Db	241	CAGCTCGAAATCGGCGAAACCCCTGATTTTACGCGAGTTTCCACAGATGATGGGA 300
Qy	301	CAAGCTTGGGGATGAAGTCCCTGCGGTATTGACACTTTGAGGGCGCGACTACTGACAGAT 360
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Db	361	GAGGGCGGATCTTGACACTTGAAGGGGAGAGTGTGACAGATGAGGGCGCACCTAT 420
Qy	421	TGACATTTGAGGGCTGTCCACAGCGCAAAATCCAGCATTTGCAAGGTTTCGCCCGT 480
Db	421	TGACATTTGAGGGCTGTCCACAGCGCAAAATCCAGCATTTGCAAGGTTTCGCCCGT 480
Qy	481	TTTTTGGCCACCGCTAACCCTGCTTTTAACTGCTTTTAAACCAATATTTATAACCTTG 540
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Qy	541	TTTTTAAACAGGGGTGGCCCTGTGCGGTGACCGCGACCGCGAGGGGGTGGCCGCC 600
Db	541	TTTTTAAACAGGGGTGGCCCTGTGCGGTGACCGCGACCGCGAGGGGGTGGCCGCC 600
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781	GGGGATAAACCGACGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGAACCGTAAA 840	Db
841	AAGGCGCGTGTGCTGGCGTTTTCATAGGCTCCGCGCCCTGACGAGCATCAAAAAT 900	Qy
841	AAGGCGCGTGTGCTGGCGTTTTCATAGGCTCCGCGCCCTGACGAGCATCAAAAAT 900	Db
901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACGAGGTTTCCC 960	Qy
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1261	AGGTAGATTTATACGAGGTATGAAACGAGAAATGGACCTTTACAGAAATCTCTATGA 1320	Db
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1441	TATGTAGGATTTTCAGGGGCAAGGATAGGCGCGCTTATCAATATATCTATAGAAT 1500	Db
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RESULT 2  
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LOCUS AX093010  
DEFINITION Sequence 15 from Patent WO0118192.  
ACCESSION AX093010  
VERSION AX093010.1 GI:13509485  
KEYWORDS synthetic construct  
SOURCE

ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 15 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)  
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RESULT 3	
AX093016	
LOCUS	Sequence 21 from Patent WO0118192.
DEFINITION	AX093016
ACCESSION	AX093016.1
VERSION	GI:13509491
KEYWORDS	synthetic construct
SOURCE	



ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Gruber,V. and Comeau,D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods  
for obtaining them  
JOURNAL Patent: WO 0118192-A 21 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)  
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7169. .7687  
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7688. .9496  
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ORIGIN

Query Match 94.7%; Score 4549; DB 6; Length 10003;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTTCCTCGCCCTGGGCTGGCGCGCTCTATGCGCCCTGCAACCGCCAG 60  
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DB 61 AAACCGCTCGAAGCGGTGTGGAGACACCGCGCGCGCGGTGTGGATACCTCGCGG 120

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QY 181 CCGCGCGGGCTTGACAGATGAGGGCGGAGCTCGATTTGGCGCGGACGTGAGCTGGC 240  
DB 181 CCGCGCGGGCTTGACAGATGAGGGCGGAGCTCGATTTGGCGCGGACGTGAGCTGGC 240

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QY 361 GAGGGCGCGATCCTTTGACACTTTGAGGGCGAGAGTCTGACAGATGAGGGCGCACCTAT 420  
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QY 421 TGACATTTGAGGGGTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCGCGCGT 480  
DB 421 TGACATTTGAGGGGTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCGCGCGT 480

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DB 481 TTTTGGCCACCGCTAACCTGCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540

QY 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAAGGGGGTGCCTCCC 600  
DB 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAAGGGGGTGCCTCCC 600

QY 601 CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA 660  
DB 601 CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA 660

QY 661 AAATACCGATACAGGGCTCTTCCGCTTCTGCTCACTGCTCACTGCTGCGTGGCTCGTGT 720  
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QY 721 CGGCTCGCGGAGCGGTATCAGCTCACTCAAGGGCGGTAAATCGGTATTCACAGAAATCA 780  
DB 721 CGGCTCGCGGAGCGGTATCAGCTCACTCAAGGGCGGTAAATCGGTATTCACAGAAATCA 780

QY 781 GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAAACCGTAA 840  
DB 781 GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAAACCGTAA 840

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DB 841 AAGGCGCGTGTGCTGGCGTTTTCATAGGCTCGCGCCCTGACGAGATCACAAAAT 900

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QY 961 CTTGGAAGCTCCCTCGTGGCGTCTCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC 1020  
DB 961 CTTGGAAGCTCCCTCGTGGCGTCTCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC 1020

QY 1021 GCTTTCTCCCTTCGGGAAAGCGTGGCGTTTCTCATAGTCTACGCTGTAGGTATCTCAGT 1080  
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QY 1081 TCGGTGTAGTGTGCTCGCTCAAGTGGGCTGTGTCAGCAAGACCCCGCTTACGCGCGAC 1140  
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DB 1261 AGGTAAGATATACCGAGGTATGAAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA 1320

QY 1321 AGCGCCATATTTAAAAAGCTACCAAGACGAAGGATGAAGAGGATGAGGAGGAGGATG 1380

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Db 1441 TATGTAAGGATTTTCAGGGGCAAGGCATAGGACGCGCGCTTATCAATATATCTATAGAAT 1500  
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Db 1681 GGAACAGTGAATTTGGAGTTCTGCTTGTATATAATTTAGCTTCTTGGGGTATCTTTAAATACT 1740  
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Db 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTTAAATAGAGATATCACCGGAATTTGAAAAA 1800  
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Db 1801 ACTGATCGAAAATATACCGCTGCTGTAAGATATACGGAAGGATGTCCTCTGCTAAGGTATA 1860  
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Db 1861 TAACTGCTGGGAGAAATGAAAACCTTATATTTAAAAATGACGACAGCGGTATATAAGG 1920  
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Qy 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC 1980  
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Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCC 1980  
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Db 2041 GGGCGATGGCGTCTTTTCTCGGAAGAGATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
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Db 2101 CGAGCTGATGCGGAGTGCACTCAGGCTCTTTTCACTCCATCGACATATCGGATGTCCTTA 2160  
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Qy 2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
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Db 2161 TACGAATAGCTTAGACAGCGCTTAGCGGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
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Db 2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCTTCTGCTCCGCTCGATCAGGAGGATAT 2460  
Qy 2461 CGGGGAAGAACAGTATGTCAGCTATTTTTTGACTTACTTGGGATCAAGCTCTATTGGGA 2520  
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Db 2461 CGGGGAAGAACAGTATGTCAGCTATTTTTTGACTTACTTGGGATCAAGCTCTATTGGGA 2520  
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Db 2521 GAAAAATAAATAATTTATTTTACTGGATGAAATGTTTTTAACTTACTAGATGTTGGCGCAACG 2580  
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Db 2581 ATGCCGCGGACAAAGCAGGAGCGACCGATCTTTTCCGCAATCAAGTGTTTTGGCTCTCAGG 2640  
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Db 3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGCGCGCGCTTGTGTAACACACGGAAGC 3240  
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Qy 3241 AGCAGATCAAGGAAATGACAGTCTTCTGTTTCCATATGCGCGCTGGCGCGACACGATGC 3300  
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Db 3241 AGCAGATCAAGGAAATGACAGTCTTCTGTTTCCATATGCGCGCTGGCGCGACACGATGC 3300  
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Qy 3361 CGCGGAGGGCGTGCAAAACAGGTCATTTTCCAGCTCAACAGGAGCTGAAGATCACCT 3420  
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Db 3421 ACACCGCGTTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480  
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Qy 3481 ACAGCAAGCGCAACCCCTATTCGCGGAGCGGATCACTTTACGTTCTACGAGCTTTGCCAGG 3540  
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Qy	3501	TACAGGCGAGCGATGGGCTTACGTCGACCGCGTGGGACCTTGGAAATCGGTGTCG	3660
Db	3601	TACAGGCGAGCGATGGGCTTACGTCGACCGCGTGGGACCTTGGAAATCGGTGTCG	3660
Qy	3661	TGCTGACCGCTTCCGGTCTTGACCGTGGCAAGAAAGTCCCGTTCAGGCTCTGA	3720
Db	3661	TGCTGACCGCTTCCGGTCTTGACCGTGGCAAGAAAGTCCCGTTCAGGCTCTGA	3720
Qy	3721	TCGACGAGGAATCGTCTGCTGTTTCTGCTGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAATCGTCTGCTGTTTCTGCTGCGACCACTACAGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAAGCTGTGCCGACCGCCGACGATGTTTTCGACTATTTTCAGCTCGACCGGG	3840
Db	3781	AGTACCGCAAGCTGTGCCGACCGCCGACGATGTTTTCGACTATTTTCAGCTCGACCGGG	3840
Qy	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACCCGCG	3900
Db	3841	AGCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACCCGCG	3900
Qy	3901	TGAAGAGTGGCGGACGAGTGGCGAAGCTTCCGAAAGTTCGAGGCGGCGCTGG	3960
Db	3901	TGAAGAGTGGCGGACGAGTGGCGAAGCTTCCGAAAGTTCGAGGCGGCGCTGG	3960
Qy	3961	TGGAACACGCTGGTCAATGATGACCTTGGTGTGATTGCAACGCTAGGCGCTTGTGGGT	4020
Db	3961	TGGAACACGCTGGTCAATGATGACCTTGGTGTGATTGCAACGCTAGGCGCTTGTGGGT	4020
Qy	4021	CAGTTCGGCTGGGTTTACGACGCGCTTCTTCTGCGATTTCTAGCTTACGCTTT	4080
Db	4021	CAGTTCGGCTGGGTTTACGACGCGCTTCTTCTGCGATTTCTAGCTTACGCTTT	4080
Qy	4081	CTGATGGCTGCCTGTATCAGTGGTGTATTTGTCGAGCTGCGGTCGGGAGCTGTT	4140
Db	4081	CTGATGGCTGCCTGTATCAGTGGTGTATTTGTCGAGCTGCGGTCGGGAGCTGTT	4140
Qy	4141	GGCTGGCTGGGAGATATTTGTTGTGTAACAAATTTAGCGCTTACAACTTAATA	4200
Db	4141	GGCTGGCTGGGAGATATTTGTTGTGTAACAAATTTAGCGCTTACAACTTAATA	4200
Qy	4201	ACACATTCGGAGCTTTTATGCTAGTGGGCTATCCCCGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTCGGAGCTTTTATGCTAGTGGGCTATCCCCGGGGATATCCATAGGCCCG	4260
Qy	4261	ATCTAGTAACATATGACCGCGCGATAATTTATCTTATCTTGTGGCGCTATATTTTG	4320
Db	4261	ATCTAGTAACATATGACCGCGCGATAATTTATCTTATCTTGTGGCGCTATATTTTG	4320
Qy	4321	TTTTCTATCCGTTATTAATGTTAAATGCGGACTTAATATATAAAACCCATCTCAT	4380
Db	4321	TTTTCTATCCGTTATTAATGTTAAATGCGGACTTAATATATAAAACCCATCTCAT	4380
Qy	4381	AATAAGCTGATGATTAATGTTAAATTTACATGCTTAACGTTAAATTCACAGAAATAT	4440
Db	4381	AATAAGCTGATGATTAATGTTAAATTTACATGCTTAACGTTAAATTCACAGAAATAT	4440
Qy	4441	ATGATTAATCATCGCAAGCGGCAACAGGATTCATCTTAAGAAACTTTATTCGCAATG	4500
Db	4441	ATGATTAATCATCGCAAGCGGCAACAGGATTCATCTTAAGAAACTTTATTCGCAATG	4500
Qy	4501	TTTGAACGATCGTTCGAGCTATGGGCCCGAAGCTTGGCCGGCCGTT	4549
Db	4501	TTTGAACGATCGTTCGAGCTATGGGCCCGAAGCTTGGCCGGCCGTT	4549

RESULT 4  
AX093011  
LOCUS

AX093011 5614 bp DNA linear PAT 30-MAR-2001

DEFINITION	Sequence 16 from Patent WO0118192.
ACCESSION	AX093011
VERSION	AX093011.1 GI:13509486
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Gruber, V. and Comeau, D.
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL	Patent: WO 0118192-A 16 15-MAR-2001;
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misc_feature	4106..4271
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terminator	4272..4559
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misc_feature	4575..5150
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ORIGIN	

Query Match 94.3%; Score 4531.4; DB 6; Length 5614;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CGGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG	60
Db	1	CGGGGCTGGTGGCCCTCGCGCTGGGCTGGCGGCGCTCTATGGCCCTGCAAGCGCCAG	60
Qy	61	AAACCGCTCGAAGCGCTGTGCGAGACACCGCGGCGCGGCTGTGGATACCTCGCGG	120
Db	61	AAACCGCTCGAAGCGCTGTGCGAGACACCGCGGCGCGGCTGTGGATACCTCGCGG	120
Qy	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180
Db	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC	180
Qy	181	CGGGCGCGGCTTACAGATGAGGGCGGACGCTGATTTTCGGCGGCGGAGCTGGC	240
Db	181	CGGGCGCGGCTTACAGATGAGGGCGGACGCTGATTTTCGGCGGCGGAGCTGGC	240
Qy	241	CAGCCTCGCAAAATCGCGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA	300
Db	241	CAGCCTCGCAAAATCGCGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA	300
Qy	301	CAGCCTCGGGATAGTGCCTCGGCTGATTTGACACTTTGAGGGGCGGACTACTGACAGAT	360
Db	301	CAAGCCTGGGATAGTGCCTCGGCTGATTTGACACTTTGAGGGGCGGACTACTGACAGAT	360

Qy	361	GAGGGCGCATCTTGACACTTGAGGGCAGAGTGTGACAGATGAGGGCGGCACCTAT	420
Db	361	GAGGGCGCCATCTTGACACTTGAGGGCGAGAGTGTGACAGATGAGGGCGGCACCTAT	420
Qy	421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCATTTGCAAGGGTTTCGGCCCGT	480
Db	421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCATTTGCAAGGGTTTCGGCCCGT	480
Qy	481	TTTTTGGCCACCGGTAACTGCTCTTTAACTGCTCTTTAAACCAATATTTATAACCTTG	540
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Qy	541	TTTTTAAACAGGCTGCGCCCTGTGCGCGTGACCGCGCACGCCGAGGGGGTGCCCCCC	600
Db	541	TTTTTAAACAGGCTGCGCCCTGTGCGCGTGACCGCGCACGCCGAGGGGGTGCCCCCC	600
Qy	601	CTTCTCGAAACCTCCCGGAAGGTATCGCGTGTGAAATACCGCACAGATCGGTAAGGAGA	660
Db	601	CTTCTCGAAACCTCCCGGAAGGTATCGCGTGTGAAATACCGCACAGATCGGTAAGGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Qy	721	CGGTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCACAGAATCA	780
Db	721	CGGTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGTTTATCCACAGAATCA	780
Qy	781	GGGGATAACCGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAACCGGTAAA	840
Db	781	GGGGATAACCGAGAAAGAACATGTAGCAAAAGGCCAGCAAAAGGCCAGGAACCGGTAAA	840
Qy	841	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAT	900
Db	841	AAGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAT	900
Qy	901	CGAGCTCAAGTCAGAGTGGCAAAACCGACAGGACTATAAGATACAGGGGTTTTCCC	960
Db	901	CGAGCTCAAGTCAGAGTGGCAAAACCGACAGGACTATAAGATACAGGGGTTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTCTGTTCCGTCGAAGCTGGGCTGTGTCACAGAACCCCGGTTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGGTCTGTTCCGTCGAAGCTGGGCTGTGTCACAGAACCCCGGTTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTGAAGACAGCTTATCG	1200
Db	1141	CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTGAAGACAGCTTATCG	1200
Qy	1201	CCACTGGAGCAGCCTTCTACCAATAATCCGGGATAAACCCAGCAACCAATTTGAGGTGAT	1260
Db	1201	CCACTGGAGCAGCCTTCTACCAATAATCCGGGATAAACCCAGCAACCAATTTGAGGTGAT	1260
Qy	1261	AGGTAAGATTATCCGAGGTATGAACGAAATTTGGACCTTTTACAGAAATTTACTCTATGA	1320
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AUTHORS Gruber,V. and Comeau,D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 3 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)  
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2604. .4098  
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## ORIGIN

Query Match 94.3%; Score 4531.4; DB 6; Length 5971;  
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AUTHORS
Gruber, V. and Comeau, D.
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ORIGIN

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Qy	2881	AGGCATACAGCAAGAACTGATTCGACCGGGTTTTTCCGCCGAGGATGCCGAAACCATCG	2940	3961	TGGAACACGGCTGGGTCAATGATGACCTGGTGCATTCGAAACGCTAGGGCTTGTGGGT	4020
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Qy	4141	GGCTGGCTGGTCGAGGATATTTGTGGTGAACAAATTTGACGCTTAGACAACTTAATA	4200
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LOCUS	AX093000	6017 bp	DNA linear PAT 30-MAR-2001
DEFINITION	Sequence 5 from Patent WO0118192.		
ACCESSION	AX093000		
VERSION	AX093000.1	GI:13509474	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Gruber, V. and Comeau, D.		
TITLE	Synthetic vectors, transgenic plants containing them, and methods for obtaining them		
JOURNAL	Patent: WO 0118192-A 5 15-MAR-2001;		
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Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGGATAAACCCAGCGAACCATTTGAGGTGAT	1260
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LOCUS AX093002 6017 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 7 from Patent WO0118192.  
ACCESSION AX093002  
VERSION AX093002.1 GI:13509476  
KEYWORDS synthetic construct  
SOURCE artificial sequences.  
ORGANISM 1  
REFERENCE 1  
AUTHORS Gruber,V. and Comeau,D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 7 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)

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VERSION AX093004.1 GI:13509478
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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gruber, V. and Comeau, D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 9 15-MAR-2001; MERISTEM THERAPEUTICS (FR)
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artificial sequences.

REFERENCE 1  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 13 15-MAR-2001;  
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ORIGIN

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ACCESSION AX093012  
VERSION AX093012.1 GI:13509487  
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SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Gruber V. and Coneau D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them  
JOURNAL Patent: WO 0118192-A 17 15-MAR-2001;  
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Sequence 19 from Patent WO0118192.			
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VERSION			
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SOURCE			
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artificial sequences.			
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AUTHORS			
Gruber V. and Comeau D.			
TITLE			
Synthetic vectors, transgenic plants containing them, and methods			
for obtaining them			
Patent: WO 0118192-A 19 15-MAR-2001;			
JOURNAL			
MERISTEM THERAPEUTICS (FR)			
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Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Qy	61	AAACCGCTCGAGCCGTGTGAGACACCGCGGCCCGCGCTTGTGGATACCTCGCG	120
Db	61	AAACCGCTCGAAGCCGTGTGAGACACCGCGGCCCGCGCTTGTGGATACCTCGCG	120
Qy	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGCGGACTCAC	180
Db	121	AAACTTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGCGGACTCAC	180
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Qy	301	CAAGCTTGGGGATAAGTGGCTCGGTATTGACACTTGAGGGCGGCGACTTACTGACAGAT	360
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Qy	361	GAGGGCGGATCCTTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGCGGCGACTTAT	420
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Qy	541	TTTTTAAACAGGGCTGGCCCTGTGCGGTGACCGCGCAGCCGAAAGGGGGTTCGCCCC	600
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Qy	781	GGGGTAAACGAGGAAAGACATGTGAGCAAAAGGCGCAGCAAGGCGCAGAAACCGTAAA	840
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Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTCCC	960
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Qy	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTCTGCTTCAAGCTGGGCTGTGTGACGAAACCCCGTTCAGCCGAC	1140
Db	1081	TCGGTGTAGGTCTGCTTCAAGCTGGGCTGTGTGACGAAACCCCGTTCAGCCGAC	1140

QY	1141	CGCTGGCCCTTATCCGGTAACATACGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCG	1200
Db	1141	CGCTGGCCCTTATCCGGTAACATACGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCG	1200
QY	1201	CCACTGGCAGCGCTTCTACCAATATCCGGTAATACCAGCAACCATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGCGCTTCTACCAATATCCGGTAATACCAGCAACCATTTGAGGTGAT	1260
QY	1261	AGGTAAGATTATACCGAGGTATGAAACAGAAATGGACCTTTACAGAAATTACTCTATGA	1320
Db	1261	AGGTAAGATTATACCGAGGTATGAAACAGAAATGGACCTTTACAGAAATTACTCTATGA	1320
QY	1321	AGGCCATATTTAAAAAGCTTACCAAGACGAAGGATGAAGAGGATGAGGAGCAGATTG	1380
Db	1321	AGGCCATATTTAAAAAGCTTACCAAGACGAAGGATGAAGAGGATGAGGAGCAGATTG	1380
QY	1381	CTTTGATATATTGACAACTACTGATAGATAATACATCTTTTATATAGAGATATCGCCG	1440
Db	1381	CTTTGATATATTGACAACTACTGATAGATAATACATCTTTTATATAGAGATATCGCCG	1440
QY	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGGCTTATCAATATATCTATAGAAT	1500
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QY	1561	CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGCTCCGTCGATATCTATGTTATAG	1620
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QY	1681	GGAACTGTAATTTGGAGTTGCTCTGTTATTAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681	GGAACTGTAATTTGGAGTTGCTCTGTTATTAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
QY	1741	GTAGAAAAGGAAGGAATAATAATGGCTAAATGAGNATATCACCGGAATTTGAAAAA	1800
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Db	2281	TGATTTTTTAAAGACGGAAACCCGAAAGAACTTGTTCTTTTCCACGGCGACCTGGG	2340
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DEFINITION Sequence 55 from Patent WO0118192.  
ACCESSION AX093050  
VERSION AX093050.1 GI:13509525  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Gruber, V. and Comeau, D.  
TITLE Synthetic vectors, transgenic plants containing them, and methods  
for obtaining them  
JOURNAL Patent: WO 0118192-A 55 15-MAR-2001;  
MERISTEM THERAPEUTICS (FR)

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ORIGIN  
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DB 1501 GGGCAAGCATAAACCTTCATGGACTAATGCTTGAACCCAGGACAATAACCTTATAG 1560  
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DB 1561 CTTGTAAATTTCTACCAAAATTTGTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG 1620  
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DB 1621 CCAACTTTGAAACAACTTTGAAAGCTGTTTTCTGGTATTTAAAGTTTGAAGTCGAA 1680  
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DB 1801 ACTGATCGAAATATACCGTGGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
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DB 1861 TAACTGGTGGGAGAAAAATGAAAACTATATTTAAAAATGACGACAGCCGGTATAAAG 1920  
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DB 1921 GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
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QY 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGAATGTCCTTA 2160  
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DB 2401 CGGCGGGCGGACAGTGTGATGACATTCGCTTCGCGTCCGTCGATCAGGGAGGATAT 2460  
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DB 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTGGGATCAAGCTGATTTGGGA 2520  
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DB 2521 GAAAATAAATAATATATTTTTTCTGATGAAATGTTTTTATAGTACCTTAGATGTGGCGAACG 2580  
QY 2581 ATGCGGCGCACAGGAGCGCACGACTCTTCGCGATCAAGTCTTTTGGCTCTCAGG 2640  
DB 2581 ATGCGGCGCACAGGAGCGCACGACTCTTCGCGATCAAGTCTTTTGGCTCTCAGG 2640  
QY 2641 CGGAGGCCACCGCAAGTATTTTGGGCAAGGGGTGCTGCTGATTTCTGTCAGGGCAAGATTCT 2700

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3121	QY	AGTCGAT	GACCAT	CGACAC	CGAGG	AAC	TATGAC	CAAGAG	CGGAAACCCGCGCG	3180	
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3181	DB	AGGACCT	GCGAAAC	CAGGT	CAG	CGAGC	CAAGCG	CGCGTTC	GCTGAACACACGAGC	3240	
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3241	DB	AGCAGAT	CAAGG	AAATGC	ACGCTT	CTCTG	TTCGAT	TTCG	CGCGTGGCGGACACGATGC	3300	
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3301	DB	GAGCGAT	GCCAAAC	CGAC	CGCGCG	CTCTG	CCCTGTTT	CAC	ACGCGCAACAAGAAATCC	3360	
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3661	QY	TGCTG	CACCGCTT	CCGCGT	CTG	GACCGT	G	GCAG	AAAAAGTCCCGTTCG	3720	
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3781	Qy	AGTACCGCAAGCTGTGCGCGACGGCCCGACGGATGTTCAGTATTTTCAGCTCGCACCGGG	384
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3961	Qy	TGGAACACCGCTGGGTCAATGATGACTGGTGCATTTGCAACCGCTAGGCGCTTGTGGGGT	4020
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4021	Db	CAGTTCGGGCTGGGGTTCAGCAGCAGCGCTTACTGCGATTTCTAGGCTGACGCTTT	4080
4081	Qy	CTGATGGGCTGCCGTGATCGAGTGGTGATTTTGTGCCGAGCTGCCGGTCGGGAGCTGTT	4140
4081	Db	CTGATGGGCTGCCGTGATCGAGTGGTGATTTTGTGCCGAGCTGCCGGTCGGGAGCTGTT	4140
4141	Qy	GGCTGGCTGGTCGACGATATATTTGGTGTGTAAACAAATTTGACGCTTAGACAACTTAATA	4200
4141	Db	GGCTGGCTGGTCGACGATATATTTGGTGTGTAAACAAATTTGACGCTTAGACAACTTAATA	4200
4201	Qy	ACACATTCGGACGTTTTTAATGACTGCGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
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4261	Db	ATCTAGTAAACATAATGACACCGCGCGATAATTTATCCTAGTTTCGCGCTATATTTTG	4320
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4321	Db	TTTTTCTATCCGATTAATATGTTAATATTCGGGACTCTAATATCAATAAAACCCATCTCATAT	4380
4381	Qy	AATPACGTCAATGATACATGTTAAATTTATTTACATGCTTAACGTAATTCACAGAAATTAT	4440
4381	Db	AATPACGTCAATGATACATGTTAAATTTATTTACATGCTTAACGTAATTCACAGAAATTAT	4440
4441	Qy	ATGATAATCATTCGAACACGGCAACAGGATTCAAATCCTTAAGAAACTTTATTCGCAAAATG	4500
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4501	Qy	TTTTGAACGATCGTTTCGTTCGAGCTATGGGCCGA	4533
4501	Db	TTTTGAACGATCGTTTCGTTCGAGCTATGGGCCGA	4533

Search completed: July 20, 2004, 16:58:01

Job time : 18119 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 07:02:45 ; Search time 1650 Seconds  
(without alignments)  
12371.268 Million cell updates/sec

Title: US-09-845-064-10  
Perfect score: 4805  
Sequence: 1 cggggctgtgcctccgc.....gagcgcttgcgacgtca 4805

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	4805	100.0	4805	4	AAF80284	Aaf80284 Nucleotid
2	4590.8	95.5	7943	4	AAF80289	Aaf80289 Nucleotid
3	4549	94.7	10003	4	AAF80295	Aaf80295 Nucleotid
4	4531.4	94.3	5614	4	AAF80290	Aaf80290 Nucleotid
5	4531.4	94.3	5971	4	AAF80277	Aaf80277 Nucleotid
6	4531.4	94.3	6016	4	AAF80280	Aaf80280 Nucleotid
7	4531.4	94.3	6016	4	AAF80278	Aaf80278 Nucleotid
8	4531.4	94.3	6017	4	AAF80281	Aaf80281 Nucleotid
9	4531.4	94.3	6017	4	AAF80279	Aaf80279 Nucleotid
10	4531.4	94.3	6767	4	AAF80282	Aaf80282 Nucleotid
11	4531.4	94.3	6865	4	AAF80287	Aaf80287 Nucleotid
12	4531.4	94.3	7503	4	AAF80291	Aaf80291 Nucleotid
13	4531.4	94.3	7503	4	AAF80293	Aaf80293 Nucleotid
14	4531.4	94.3	8654	4	AAF80288	Aaf80288 Nucleotid
15	4531.4	94.3	8987	4	AAF80296	Aaf80296 Nucleotid
16	4531.4	94.3	9143	4	AAF80286	Aaf80286 Nucleotid
17	4531.4	94.3	9390	4	AAF80294	Aaf80294 Nucleotid
18	4528.2	94.2	8654	4	AAF80285	Aaf80285 Nucleotid
19	4528.2	94.2	9390	4	AAF80292	Aaf80292 Nucleotid
20	4519.4	94.1	6766	4	AAF80283	Aaf80283 Nucleotid
21	4070	84.7	4098	4	AAF80276	Aaf80276 Nucleotid
22	2880	59.9	3508	4	AAF80275	Aaf80275 Nucleotid
23	2536.2	52.8	12079	6	ABV74271	Abv74271 Plant spe

24	2536.2	52.8	12079	6	ABQ76793	Abq76793 pUC19 pro	
25	2536.2	52.8	12085	6	ABV74270	Abv74270 Plant spe	
26	2536.2	52.8	12085	6	ABQ76792	Abq76792 pUC19 pro	
27	2536.2	52.8	12093	6	ABV74269	Abv74269 Plant spe	
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29	2536.2	52.8	12241	6	AAQ36732	Aad36732 Binary ve	
C	30	2536.2	52.8	12241	6	ABQ73049	Abq73049 Tomato an
C	31	2536.2	52.8	13002	6	ABV74272	Abv74272 Plant spe
	32	2536.2	52.8	13002	6	ABQ76794	Abq76794 pUC19 pro
	33	2536.2	52.8	13905	6	ABV74273	Abv74273 Plant spe
	34	2536.2	52.8	13905	6	ABQ76795	Abq76795 pUC19 pro
	35	2536.2	52.8	14446	6	AAQ36732	Aad36732 Binary ve
	36	2536.2	52.8	15430	6	ABV74274	Abv74274 Plant spe
	37	2536.2	52.8	15430	6	ABQ76796	Abq76796 pB-DHGLA
	38	2536.2	52.8	17752	6	ABV74275	Abv74275 Plant spe
	39	2536.2	52.8	17752	6	ABQ76797	Abq76797 pBARA1 en
	40	2536.2	52.8	19705	6	ABA92074	Abq92074 Vector pl
C	41	2536.2	52.8	20119	4	AAH26041	Aah26041 plasmid p
	42	2536.2	52.8	20174	6	ABA92073	Abq92073 Transform
C	43	2536.2	52.8	26019	4	AAH26040	Aah26040 plasmid p
	44	2522.2	52.5	13737	3	AAA54212	Aaa54212 Transform
C	45	1496	31.1	15676	3	AAQ01288	Aad01288 Arabidops

ALIGNMENTS

RESULT 1	
ID	AAF80284 standard; DNA; 4805 BP.
XX	XX
AC	AAF80284;
DT	29-JUN-2001 (first entry)
XX	XX
DE	Nucleotide sequence of plasmid pMR1191.
KW	Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW	P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX	XX
OS	Synthetic.
XX	XX
Key	Location/Qualifiers
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FT	655. .1283
FT	rep_origin
FT	/*tag= b
FT	/*note= "ori Cole1"
FT	1264. .2603
FT	CDS
FT	/*tag= c
FT	/*note= "NPT III gene coding for neomycin
FT	phosphotransferase and kanamycin resistance"
FT	2604. .4098
FT	CDS
FT	/*tag= d
FT	/*note= "TrfA locus from RK2 coding for two proteins P285
FT	and P382 enabling an increase in the replication rate"
FT	4106. .4271
FT	misc_feature
FT	/*tag= e
FT	/*note= "T-DNA left border"
FT	4272. .4559
FT	terminator
FT	/*tag= f
FT	/*note= "nopaline synthetase terminator"
FT	4525. .4798
FT	misc_feature
FT	/*tag= g
FT	/*note= "T-DNA right border"
FT	FR2798139-A1.
PN	FR2798139-A1.
XX	XX
PD	09-MAR-2001.
XX	XX
PF	03-SEP-1999;
XX	99FR-00011112.
XX	XX



Db 1681 ||||| GGAACAGTGAATTGGAGTTCGTCTGTATATAATTAGCTTCTGGGTAATCTTTAAATACT 1740

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Db 1741 GTAGAAAAGAGGAAGAAAATAATAATGCTTAAATGAGAAATATCACCGAAATTGAAAAA 1800

Qy 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA 1860

Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTAAGGTATA 1860

Qy 1861 TAAGCTGGTGGGAGAAAATGAAAACCTATATATTTAAAAATACCGACAGCCGGTATAAAG 1920

Db 1861 TAAGCTGGTGGGAGAAAATGAAAACCTATATTTAAAAATGACGACAGCCGGTATAAAG 1920

Qy 1921 GACCACCTATGATGTGGAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC 1980

Db 1921 GACCACCTATGATGTGGAACGGGAAAGGACATGATCTATGCTGGAAGGAAAGCTGCC 1980

Qy 1981 TGTTCCAAAGGTCCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040

Db 1981 TGTTCCAAAGGTCCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040

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Db 2041 GGCGGATGGCGTCTTGTCTCGGAAGAGTATGAAGTGAACAAAGCCCTGAAAAGATTAT 2100

Qy 2101 CGAGCTGTATGCGGAGTGCAATCAGGCTCTTCACTCCATCGACATATCGGATTTGCCCTA 2160

Db 2101 CGAGCTGTATGCGGAGTGCAATCAGGCTCTTCACTCCATCGACATATCGGATTTGCCCTA 2160

Qy 2161 TACGAATAGCTTAGACACGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220

Db 2161 TACGAATAGCTTAGACACGCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220

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Qy 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATGCGGAAACCATCG 2940

Db 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATGCGGAAACCATCG 2940

Qy 2941 CAAAGCCGACCGTCATGCGTGGCCCGCGGAAACCTTCCAGTCCGCTCGGCTCGATGCTCC 3000

Db 2941 CAAAGCCGACCGTCATGCGTGGCCCGCGGAAACCTTCCAGTCCGCTCGGCTCGATGCTCC 3000

Qy 3001 AGCAAGCTACGGCAAGATCGAGCGGACAGCGGTGCAACTGGGCTCCCTCGCCCTGCGCCG 3060

Db 3001 AGCAAGCTACGGCAAGATCGAGCGGACAGCGGTGCAACTGGGCTCCCTCGCCCTGCGCCG 3060

Qy 3061 CGCCATCGGCGCGCGTGGAGCGTTTCGCGTCTCGAACAGGAGCGGCAAGTTTGGCGA 3120

Db 3061 CGCCATCGGCGCGCGTGGAGCGTTTCGCGTCTCGAACAGGAGCGGCAAGTTTGGCGA 3120

Qy 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCCGGCG 3180

Db 3121 AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGGAAACCGCCGGCG 3180

Qy 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAAGCAGGCCGCTTGTGTAACACACAGAAAGC 3240

Db 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCCAAAGCAGGCCGCTTGTGTAACACACAGAAAGC 3240

Qy 3241 AGCAGATCAAGGAAATGCAAGCTTTCTTGTTCGATATTGGCGCTGGCGGACACGATGC 3300

Db 3241 AGCAGATCAAGGAAATGCAAGCTTTCTTGTTCGATATTGGCGCTGGCGGACACGATGC 3300

Qy 3301 GAGCGATGCAAAACGACACGCGCCGCTCTGCCCTGTTTCAACGCGCGCAACAGAAATTC 3360

Db 3301 GAGCGATGCAAAACGACACGCGCCGCTCTGCCCTGTTTCAACGCGCGCAACAGAAATTC 3360

Qy 3361 CGCGCAGCGCTGCAAAACAAAGGTCATTTTCCACGTCAACAGGACGTCGAAGATCACCT 3420

Db 3361 CGCGCAGCGCTGCAAAACAAAGGTCATTTTCCACGTCAACAGGACGTCGAAGATCACCT 3420

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Db 3421 ACACCGCGCTCGAGCTGCGGGCGGACGATGACGAACTGGTGCGCAGCAGGTGTGAGT 3480

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Db 3481 AGCGAAGCGCACCCCTATCGGGAGCCGATCACCTTCACTGTTCTACGAGCTTTGCCAGG 3540

Qy 3541 ACCTGGCTGGTTCGATCAATGGCCGCTATTACACGAAGCCGAGGAATGCCTGTCGCGCC 3600

Db 3541 ACCTGGCTGGTTCGATCAATGGCCGCTATTACACGAAGCCGAGGAATGCCTGTCGCGCC 3600

Qy 3601 TACGCGCAGCGCGATGGCTTTCACGTCGCAACGCGCTTGGGCACTTGGAAATCGGTGTCG 3660

Db 3601 TACGCGCAGCGCGATGGCTTTCACGTCGCAACGCGCTTGGGCACTTGGAAATCGGTGTCG 3660

Qy 3661 TGTGTACCGCTTCCGCTCTGGACCGGTGGCAAGAAACGTCGCCCTTGGCAGGTCCTGA 3720

Db 3661 TGTGTACCGCTTCCGCTCTGGACCGGTGGCAAGAAACGTCGCCCTTGGCAGGTCCTGA 3720

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Db 3721 TCGACGAGGAAATCGTCGTGCTTTTGTGGGACCACTACAGAAATTCATATGGGAGA 3780

Qy 3781 AGTACCGCAAGCTGTGCGCGACGGCCGACGGATGTTTCGACTATTTTTCAGCTCGCACCGGG 3840

Db 3781 AGTACCGCAAGCTGTGCGCGACGGCCGACGGATGTTTCGACTATTTTCAGCTCGCACCGGG 3840

Qy 3841 AGCCGTACCCGCTCAAGCTGGAAAACCTTCCGCTCATGTGCGGATCGGATTTCCACCCGCG 3900

Db 3841 AGCCGTACCCGCTCAAGCTGGAAAACCTTCCGCTCATGTGCGGATCGGATTTCCACCCGCG 3900

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Qy 3961 TGAACACAGCTGGTCAATGATGACCTGCTGGTGCATTGCAAAAGCTAGGGCTTTGTGGGT 4020
Db 3961 TGAACACAGCTGGTCAATGATGACCTGCTGGTGCATTGCAAAAGCTAGGGCTTTGTGGGT 4020
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Db 4021 CAGTTCGGCTGGGGTTACGACGCCACGCGTTTACTGGCATTTCTTAGTTCGACGTCCT 4080
Qy 4081 CTGATGGGCTGCCTGTATCAGATGGTGATTTTGTGCGGAGCTGCGGTCCGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCTGTATCAGATGGTGATTTTGTGCGGAGCTGCGGTCCGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGCGAGGATATATTGCTGTGAACAAATTCAGCTTAGACAATTAATA 4200
Db 4141 GGCTGGCTGGCGAGGATATATTGCTGTGAACAAATTCAGCTTAGACAATTAATA 4200
Qy 4201 ACACATTGCGGACGTTTTTAATGTACTGGGCTATCCCGGGGATATCATAGGCCCG 4260
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Qy 4261 ATCTAGTAACATAATGACACGCGCGGATTAATTTATCTAGTTTGGCGGTATATTTTG 4320
Db 4261 ATCTAGTAACATAATGACACGCGCGGATTAATTTATCTAGTTTGGCGGTATATTTTG 4320
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Db 4321 TTTTCTATCGGTATTAATGATAATTTGGGGACTCTAATCATATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTCATGCAATTACATGTTAATTAATTAATCATGCTTAACGTAATTAACAGAAATAT 4440
Db 4381 AATAACGTCATGCAATTACATGTTAATTAATTAATCATGCTTAACGTAATTAACAGAAATAT 4440
Qy 4441 ATGATAATCATCGCAAGACCGGCAACAGGATTAATTAATTAAGAACTTATTCGCAATG 4500
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Db 4681 TTATTAGAATAATCGGATATTTAAAGGGCGTAAAGGTTTATCCGTTCTGTCATTTGT 4740
Qy 4741 ATGTGATGCCAACACAGGGTTTTACCGGTTTCTTAGGAAAGACCGAGCGCTTTGGGAC 4800
Db 4741 ATGTGATGCCAACACAGGGTTTTACCGGTTTCTTAGGAAAGACCGAGCGCTTTGGGAC 4800
Qy 4801 GCTCA 4805
Db 4801 GCTCA 4805
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## RESULT 2

AAF80289

ID AAF80289 standard; DNA; 7943 BP.

XX

AC

AAF80289;

XX

DT

29-JUN-2001 (first entry)

```
XX Nucleotide sequence of plasmid pMRT1201.
DE
XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
KW
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT rep_origin 1..654
FT /tag= a
FT /note= "ori RK2"
FT rep_origin 655..1263
FT /tag= b
FT /note= "ori ColE1"
FT CDS 1264..2603
FT /tag= c
FT /note= "NPT III gene coding for neomycin
FT phosphotransferase and kanamycin resistance"
FT CDS 2604..4098
FT /tag= d
FT /note= "TrfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
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FT /note= "T-DNA left border"
FT terminator 4272..4559
FT /tag= f
FT /note= "nopaline synthetase terminator"
FT promoter 4612..5047
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FT /note= "wheat high molecular weight glutenin promoter"
FT intron 5096..5627
FT /tag= h
FT /note= "rice actin intron"
FT CDS 5628..7436
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FT /note= "GUS gene coding for beta glucuronidase"
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FT misc_feature 7763..7936
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FT /note= "T-DNA right border"
XX
XX FR2798139-A1.
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 137-140; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from PRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.
```



Qy	2041	GGCGGATGGCGTCTCTTGGCTCGGAAGAGTATGAAGATGAACAAGCCCTGAAAGATTAT	2100
Db	2041		
Qy	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTGTCCCTA	2160
Db	2101		
Qy	2161	TACGAATAGCTTACAGACGCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161		
Qy	2221	CGATGTGGATTGCGAAACTCGGGAAGACACATCCCAATTAAGATCCGCGGAGCTGTA	2280
Db	2221		
Qy	2281	TGATTTTTTAAAGACGGAAAGCCGGAAGAGAACTTGTCTTTTCCACGCGACCTGGG	2340
Db	2281		
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAGTAAAGTGGCTTTATTGATCTTGGGGAAG	2400
Db	2341		
Qy	2401	CGGAGGCGGACAAAGTGGTATGACATTCGCTTCGCGTCGGATCAGGAGGATAT	2460
Db	2401		
Qy	2461	CGGGGAAGAACAGTATCTCGAGCTATTTTTTGTACTTACCTGGGATCAAGCTGATGGGA	2520
Db	2461		
Qy	2521	GAAATAAAAATATATATTTTACTTGGATGAATTTTGTAGTACTAGATGTGGCGAACG	2580
Db	2521		
Qy	2581	ATGCGCGGCAACAGCAGGCGGACCGACTCTTCCGCATCAAGTGTTTGGCTCTCAGG	2640
Db	2581		
Qy	2641	CCGAGGCCACCGCAAGTATTTTGGGCAAGGGTGCCTGCTATTCGTGAGGGCAAGATTC	2700
Db	2641		
Qy	2701	GGATACCAAGTACGAGAAGGACGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
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Qy	2761	AGGTGGATTATCTGGACACCAAGGCGACAGCGGGTCAAAATCAGGAATNAGGCGACATTG	2820
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Qy	2821	CCCCGGGTGAGTCGGGGCAATCCCGCAAGAGGAGTGAATCAATCGGACGTTTGACCGGA	2880
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Qy	2881	AGGCATACAGCAAGAATACTGATCGACGCGGGTTTTCCGCGGAGGATGCCGAAACCATCG	2940
Db	2881		
Qy	2941	CAAGCCGACCGTATCGCTGCGCGCCCGGAAACCTTCCAGTCCGTCCGATCGTCC	3000
Db	2941		
Qy	3001	AGCAAGCTACGGCCAAAGATCCAGCGGACGCTGCAACTGGCTCCCCCTGCCCTGCCCG	3060
Db	3001		
Qy	3061	CGCCATCGGCGCGGTGGAGCGTTTCGCGTCTCGAAACAGGAGCGCGAGTTTGGCGA	3120
Db	3061		

Qy	3121	AGTCGATGACCATCGACAGCGAGGAACTATGACGACCAAGAGCGAAACCCCGCGG	3180
Db	3121		
Qy	3181	AGGACCTGGCAAAACAGGTCAAGGCGCAAGCGCGCGGTTGCTGAAACACACGAAGC	3240
Db	3181		
Qy	3241	AGCAGATCAAGGAAATGCGACTTTCCTTTCGATATTGCGCGTGGCGGACACCATGC	3300
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Qy	3301	GAGCGATGCCAAACGACACGCGCGCTCTGCGCTGTTCAACGCGCAACAGAAATCC	3360
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Qy	3361	CGCGAGGCGCTGCAAAAACAAAGTCAATTTTCCACGTCAACAGGACGTTGAAGATCACCT	3420
Db	3361		
Qy	3421	ACACCGCGTCGAGCTGCGGGCGGATGACGAACTGGTGTGGCAGCAGGTCTTGAGT	3480
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Db	3481		
Qy	3541	ACCTGGCTGGTTCGATCAATGGCCGGTATTACAGGAAGCCGAGGAATGCTCTGCGGCC	3600
Db	3541		
Qy	3601	TACAGGAGCGGATGGGCTTCACTCCGACCGCTTGGGCACTTGGCACTCGGTGTCG	3660
Db	3601		
Qy	3661	TGCTGCAACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGTCCTGTCAGGCTCTGA	3720
Db	3661		
Qy	3721	TCGACGAGGAAATGCTGCTGCTTTGCTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721		
Qy	3781	AGTACCGCAGCTGTCGCGACCGCGCGAGCGGATGTTTCACTATTTTCACTCGCACCGGG	3840
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Qy	3841	AGCGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCCACCCGCG	3900
Db	3841		
Qy	3901	TGAAGAAGTGGCGAGCAGGTGCGGCAAGCTTGGCAAGAGTTGCGAGGCGAGCGGCTTG	3960
Db	3901		
Qy	3961	TGGNACACGCTGGGCTCAATGATGACTGGTGCATTTGCAAAACGCTAGGGCTTGTGGGT	4020
Db	3961		
Qy	4021	CAGTTCGGCTGGGGTTTACGACGCGCTTTTACTGGCATTTTCTAGGTTGACGCTTT	4080
Db	4021		
Qy	4081	CTGATGGGCTGCTGTATCGAGTGGTGAATTTGTGCGGAGCTGCGGTCGGGGAGCTGTT	4140
Db	4081		
Qy	4141	GGCTGGCTGGCGAGATATATTGGTGTAAACAAATTTAGCGCTTAGACAACTTAATA	4200
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Db 4261 |ATCTAGTAACATAATGACACCGCGCGGATAAATTTATCTAGTTTGGCGCTATATTTTG 4320
Qy 4321 |TTTTCTATCGGTATTAATGATGATAATTTGGGGACTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 |TTTTCTATCGGTATTAATGATGATAATTTGGGGACTCTAATCATATAAAACCCATCTCAT 4380
Qy 4381 |AATAAGTCATGATACATGTTAATTTATTTACATGCTTAACGTTAATTTCAACAGAAATTAT 4440
Db 4381 |AATAAGTCATGATACATGTTAATTTATTTACATGCTTAACGTTAATTTCAACAGAAATTAT 4440
Qy 4441 |ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTTATTCGCAATG 4500
Db 4441 |ATGATAATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTTATTCGCAATG 4500
Qy 4501 |TTTGAACGATCGTTCTGCGAGCTATGGGCCCGAAGCTTTGGCCGCCGTTAACACGCGTGG 4560
Db 4501 |TTTGAACGATCGTTCTGCGAGCTATGGGCCCGAAGCTTTGGCCGCCGTTAACACGCGTGG 4560
Qy 4561 |ATCCTTAATTAAGTCGACTCTAGAGAAATTCAC 4594
Db 4561 |ATCCTTAATTAAGTCGACTCTAGAGAAATTAATTC 4594

RESULT 3
AAF80295
ID AAF80295 standard; DNA; 10003 BP.
AC AAF80295;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMRT1210.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX Synthetic.
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FT and P382 enabling an increase in the replication rate"
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FN FR2798139-AL.
XX
PD 09-MAR-2001.
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PF 03-SEP-1999; 99FR-00011112.
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PR 03-SEP-1999; 99FR-00011112.
XX
PA (MERI-) MERISTEM THERAPEUTICS SA.
XX
PI Gruber V, Comeau D;
XX
DR WPI; 2001-259847/27.
XX
PT New vector free from non-essential elements, useful for transforming
PT cells for protein production and for preparing transgenic plants.
XX
PS Claim 20; Page 163-166; 180pp; French.
XX
CC The specification describes a synthetic vector containing only those
CC elements essential for its functionality and transgenesis of a cell
CC (especially a plant cell). The vector consists of at most one origin of
CC replication (ori), at most one sequence encoding a selection agent and a
CC trfA locus encoding a protein that increases the level of plasmid
CC replication. The vector particularly contains an RK2 ori, especially oriV
CC from pRK2 of Escherichia coli with a broad host range, an antibiotic
CC resistance gene (especially nptII conferring resistance to kanamycin in
CC bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
CC The vectors are used to prepare transgenic plants and transformed host
CC cells for production of a heterologous proteins, e.g. insulin,
CC interferon, lipase, blood proteins and anti-inflammatory agents. The
CC present sequence represents a plasmid of the invention
XX
SQ Sequence 10003 BP; 2476 A; 2470 C; 2729 G; 2328 T; 0 U; 0 Other;

Query Match 94.7%; Score 4549; DB 4; Length 10003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGCTGTTGCCCTCGCGCTGGCGCTGGCGCTGCTATGSCCTTGCAACGCGCCAG 60
Db 1 CCGGGCTGTTGCCCTCGCGCTGGCGCTGGCGCTGCTATGSCCTTGCAACGCGCCAG 60
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Db 61 AAACGCGCTCGAAGCCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCG 120
Qy 121 AAACCTTGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC 180
Db 121 AAACCTTGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC 180
Qy 181 CCGGCGCGCGTGTGACAGATGAGGGCGGACGTTGCTGATTCGGCGCGGCGAGTGGCGTGGC 240
Db 181 CCGGCGCGCGTGTGACAGATGAGGGCGGACGTTGCTGATTCGGCGCGGCGAGTGGCGTGGC 240
Qy 241 CAGCCTCGCAAAATCGGGCAAAACGCCCTGATTTTACGCGAGTTTCCCAAGATGATGTGGA 300
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241	Db		CAGCCTCGCAAAATCGGCGAAAA	CGCCTGATTTTACGCGAGT	TTTCCACAGATGATGTGGA	300
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301	Db		CAAGCCTGGGGATAAGTGCCTCGGTATTTGACACTTTAGGGGCGGAGTACTTGACAGAT			360
361	Qy		GAGGGGCGGATCCTTCACACTTCGAGGGGAGAGTGTGACAGATGAGGGGCGCACCTAT			420
361	Db		GAGGGGCGGATCCTTCGACACTTCGAGGGGAGAGTGTGACAGATGAGGGGCGCACCTAT			420
421	Qy		TGACATTTGAGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTGAAGGGTTTCGGCCCGT			480
421	Db		TGACATTTGAGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTGAAGGGTTTCGGCCCGT			480
481	Qy		TTTTTGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG			540
481	Db		TTTTTGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG			540
541	Qy		TTTTTTAACACAGGGCTGCGCGCTGACCGCGTGAACCGCAACCGGAGGGGGTGC			600
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601	Qy		CTTCTCGAAACCTCCCGGAAAGGTATCGGGTGTGAAATACCGCACAGATCGTAAAGGAGA			660
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661	Qy		AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGCTT			720
661	Db		AAATACCGCATCAGGCGCTCTTCGGCTTCTCGCTCACTGACTCGCTGCGCTCGGTGCTT			720
721	Qy		CGGCTGCGGAGCGGTATCAGCTCACTCAAAGSCGGTAAATACGGTTATCCACAGAAATCA			780
721	Db		CGGCTGCGGAGCGGTATCAGCTCACTCAAAGSCGGTAAATACGGTTATCCACAGAAATCA			780
781	Qy		GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCAGGAACCGTAAA			840
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901	Qy		CGAGCTCAAGTCAGAGGTGCGGAAACCCGACAGAGCTATAAAGATACACAGGCGTTTCCC			960
901	Db		CGAGCTCAAGTCAGAGGTGCGGAAACCCGACAGAGCTATAAAGATACACAGGCGTTTCCC			960
961	Qy		CCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCC			1020
961	Db		CCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCC			1020
1021	Qy		GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGT			1080
1021	Db		GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGT			1080
1081	Qy		TCGGGTAGGTCTGCTTCCGCTCAAGCTGGGCTGTGTCAGCAACCCCGCTTCAGCCCGAC			1140
1081	Db		TCGGGTAGGTCTGCTTCCGCTCAAGCTGGGCTGTGTCAGCAACCCCGCTTCAGCCCGAC			1140
1141	Qy		CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGCACGACTTATCG			1200
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1201	Qy		CCACTGGCAGCGCTTCTACCAATAATCCGGGATAAACCCAGCGAAACATTTGAGGTGAT			1260
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1261	Qy		AGGTAAAGATTATACCGAGGTATGAAACCGAGAAATGGACCTTTTACAGAAATTTACTATGA			1320
1261	Db		AGGTAAAGATTATACCGAGGTATGAAACCGAGAAATGGACCTTTTACAGAAATTTACTATGA			1320
1321	Qy		AGCGCCCATATTTAAAAAGCTACCAAGACGAAAGAGGATCAAGAGATGAGGAGCGAGTTG			1380

Db	1321	AGCCCCATATTTAAAAAGCTTACCAAGACGAAAGGATGAAGAGGATGAGGAGCGCAGATTG	1381
Qy	1381	CTTTGAATATATTGACAATACTCATAGATAATAACATCTTTTATATAGAAGATATCGCCG	1440
Db	1381	CTTTGAATATATTGACAACTCATAGATAATAACATCTTTTATATAGAAGATATCGCCG	1440
Qy	1441	TATGTAAGGATTTTCAGGGGCAAGGATAGGACAGCGCTTATCAATATATCTATAGAAT	1500
Db	1441	TATGTAAGGATTTTCAGGGGCAAGGATAGGACAGCGCTTATCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAGCATAAAACTTCATGGACTAATGCTTGAAACCCAGGACAAATAAACCCTTATAG	1560
Db	1501	GGGCAAGCATAAAACTTCATGGACTAATGCTTGAAACCCAGGACAAATAAACCCTTATAG	1560
Qy	1561	CTTTGTAATTTCTACCAAAATTTGTGGTTTCAAAATCGGCTCGATCTATGTTATACG	1620
Db	1561	CTTTGTAATTTCTACCAAAATTTGTGGTTTCAAAATCGGCTCGATCTATGTTATACG	1620
Qy	1621	CCAACCTTTGAAAAACAACCTTTGAAAAAGCTGTGTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Db	1621	CCAACCTTTGAAAAACAACCTTTGAAAAAGCTGTGTTTCTGGTATTTAAGGTTTTAGAAATGCAA	1680
Qy	1681	GGAAACAGTGAATTTGGAGTTTCGTTCTGTTATAATTAGCTTCTCGGGGTATCTTTAAATACT	1740
Db	1681	GGAAACAGTGAATTTGGAGTTTCGTTCTGTTATAATTAGCTTCTCGGGGTATCTTTAAATACT	1740
Qy	1741	GTAGAAAGAGGAGGAATAATAAATGGCTAAAAATGAGAAATCACCGGAAATTTGAAAAA	1800
Db	1741	GTAGAAAGAGGAGGAATAATAAATGGCTAAAAATGAGAAATCACCGGAAATTTGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTCGCTAAAGATACGGAAGGAATGTCTCTCTCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTCGCTAAAGATACGGAAGGAATGTCTCTCTCTAAGGTATA	1860
Qy	1861	TAAGCTGCTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGACAGCCGGTATAAAGG	1920
Db	1861	TAAGCTGCTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGACAGCCGGTATAAAGG	1920
Qy	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
Db	1921	GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGTCCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA	2040
Db	1981	TGTTCCAAAGGTCCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA	2040
Qy	2041	GGCCGATGGCGTCCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
Db	2041	GGCCGATGGCGTCCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
Qy	2101	CGAGCTGATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGAATGTCCCTTA	2160
Db	2101	CGAGCTGATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGAATGTCCCTTA	2160
Qy	2161	TACGAATAGCTTAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGTAATACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGTAATACGATCTGGC	2220
Qy	2221	CGATGTGGATTGGAAAACTTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA	2280
Db	2221	CGATGTGGATTGGAAAACTTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGGAAGCCCGAAGAGGAACCTTGCTTTTCCACGCGCAGCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAGCCCGAAGAGGAACCTTGCTTTTCCACGCGCAGCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGSCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGSCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Qy	2401	CGGAGGGCGGACAAAGTGGTATGACATTTGCTTCTCGGTCGATCAGGAGGATAT	2460
Db	2401	CGGAGGGCGGACAAAGTGGTATGACATTTGCTTCTCGGTCGATCAGGAGGATAT	2460



QY	2461	CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTGGGATCAAGCTGATTGGGA	2520
DB	2461		
QY	2521	CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTGGGATCAAGCTGATTGGGA	2520
DB	2521		
QY	2521	GAAAAAATAATATATTTTACTGAGATGAATTTGTTTGTAGTACTAGATGTGGCGAAGC	2580
DB	2521		
QY	2581	GAAAAAATAATATATTTTACTGAGATGAATTTGTTTGTAGTACTAGATGTGGCGAAGC	2580
DB	2581		
QY	2581	ATCGCGCGAAGCAGGAGCGACCGACTTCTCCGCATCAAGTGTGTTGGCTCTCAGG	2640
DB	2581		
QY	2641	ATCGCGCGAAGCAGGAGCGACCGACTTCTCCGCATCAAGTGTGTTGGCTCTCAGG	2640
DB	2641		
QY	2641	CCGAGGCCCAAGCAAGTATTTGGGCAAGGGGTCGCTGATTCGTGCGAGCGCAAGATTC	2700
DB	2641		
QY	2701	CGAGGCGCAAGCAAGTATTTGGGCAAGGGGTCGCTGATTCGTGCGAGCGCAAGATTC	2700
DB	2701		
QY	2701	GGAAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCAATGGCGATA	2760
DB	2701		
QY	2761	AGGTGGATTATCTGGACACCAAGGCACAGGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
DB	2761		
QY	2821	CCCGCGCGTGAAGTCCCGCAAGGAGGGTGAATGAATCGGACGTTTGAACCGGA	2880
DB	2821		
QY	2881	AGGCATACAGGCAAGAACTGATCGACGGGGTTTTCCGCGGAGGATGCCGAAACCATCG	2940
DB	2881		
QY	2941	CAAGCGCACCGTATCGTGGCGCGCGGAACTTCCAGTCCGTCGGCTCGATGGTCC	3000
DB	2941		
QY	3001	AGCAAGCTACGGCAAGATCGAGCGGACACGCTGCAACTGGCTCCCTCGCTCGCCCG	3060
DB	3001		
QY	3061	CGCCATCGCGCGCGTGGAGCGTTCCGTCGTCGTAACAGGAGGCGGACAGGTTGGCGA	3120
DB	3061		
QY	3121	AGTCGATGACCATCGACACGAGGAACTATGACGACCAAGAAAGCGGAAACCGCGGCG	3180
DB	3121		
QY	3181	AGGACCTGGCAAAACAGGTGAGCGGCGCAAGCGCGGTTGCTGAAACACACGAAGC	3240
DB	3181		
QY	3241	AGCAGATCAAGGAAATGCAAGTTTCTTGTTCGATATTCGCGCGTGGCGGACACGATGC	3300
DB	3241		
QY	3301	GAGCGATGCCAAAGCACAGCGCGCTCTGCTGCTGTTTCCACGCGCGCAAGAAATCC	3360
DB	3301		
QY	3361	CGCGGAGGCGTGCAAAACAAGTCAATTTTCCAGCTCAACAGGACGTGAAGATCACCT	3420
DB	3361		
QY	3421	ACACCGCGTCGAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTTGGAGT	3480
DB	3421		
QY	3481	ACCGGAAGCGCACCCCTATCGGCGAGCGGATCACTTACGTTCTACGAGCTTTGCCAGG	3540
DB	3481		

QY	3541	ACCTGGCTGGTCGATCAATGGCCGGTATTTACAGGAAGCCGAGGAATGCTGTGCGGCC	3600
DB	3541		
QY	3601	TACAGCGACGGCGATGGGCTTACGTCGACCGCGTGGGCACTTGGGAATCGGTGTGCG	3660
DB	3601		
QY	3661	TGCTGCACCGCTTCCGCTCCGAGCGGTGGCAAGAAACGTCCTGTTGCCAGGCTCTGA	3720
DB	3661		
QY	3721	TCGACGAGGAAATCGTCGTGCTGTTTGTGCGGACCACTACACGAAATTCATATGGGAGA	3780
DB	3721		
QY	3781	AGTACCGCAAGCTGTCCGCGACGGCCCGAGCTGTTGCGACTATTTTCAGCTCGACCGGG	3840
DB	3781		
QY	3841	AGCCGTACCGCTCAAGCTGGAAACCTTCGCGCTCATGTGCGGATCGGATTTCCACCGCG	3900
DB	3841		
QY	3901	TGAAGAAGTGGCGGACGAGCTGGCGAAGCCTTCGGAAGATTTGCGAGGCGAGCGGCTGG	3960
DB	3901		
QY	3961	TGGAACACCGCTGGGTCATGATGACTGGTGCATTTGCAAAACGCTAGGGGCTTTGTTGGGT	4020
DB	3961		
QY	4021	CAGTTCGGCTGGGGTTCAGCAGCGAGCGCTTTTACTGCGCATTTCTTAGGTTCACGCTTT	4080
DB	4021		
QY	4081	CTGATGGGCTGCCGTATCGAGTGGTGAATTTGTGCGGAGCTGCCGCTCGGGAGCTGTT	4140
DB	4081		
QY	4141	GGCTGGCTGGTCAGGATATATTTGGTGTGTAACAAATTTGACGCTTAGACAACTTAATA	4200
DB	4141		
QY	4201	ACACATTCGGGAGCTTTTAAATGCTACTGGGCTATCCCGGGGATATCCATAGGCCCG	4260
DB	4201		
QY	4261	ATCTAGTAACATAATGACACCGCGCGATAATTTATCTAGTTTCGGGCTATATTTTG	4320
DB	4261		
QY	4321	TTTTCTATCGGTAATTAATGATATATTTGGGACTCTAATCATATAAAACCCATCTCAT	4380
DB	4321		
QY	4381	ATAACGTCATGCAATTCATGTTAATTTATACATGCTTAACGTAATTCACAGAAATAT	4440
DB	4381		
QY	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCATCTTTAAGAAACTTTATTCGCAAAATG	4500
DB	4441		
QY	4501	TTTGAACGATCGTTCGTGAGCTATGGGCCCGAAGCTTGGCGGCCGCTT	4549
DB	4501		

RESULT 4  
AAF80290  
ID AAF80290 standard; DNA; 5614 BP.  
XX



QY	961	CCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTCTGGCGCTTACCGGATACCTGTCC	1020
Db	961		
QY	1021	GCCTTTCTCCCTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTCTAGGTATCTCAGT	1080
Db	1021		
QY	1081	TCGGTGTAGGTCTGTTCCGCTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCGAC	1140
Db	1081		
QY	1141	CGCTGGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCG	1200
Db	1141		
QY	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGGATAAACCCAGCGAACCATTTGAGGTGAT	1260
Db	1201		
QY	1261	AGGTAAGATTATACCGAGGTATGAAAAACGAGAAATTGGACCTTTACAGAAATTACTCTATGA	1320
Db	1261		
QY	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGCAGATTG	1380
Db	1321		
QY	1381	CCTTGAATATATTGACAAATCTGNTAAGATAATACATCTTTTATATAGAAGATATCGCCG	1440
Db	1381		
QY	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGCGAGCGCTTATCAATATATCTATAGAAT	1500
Db	1441		
QY	1501	GGGCAAGCATAAAACTTCGATGGAATAATGCTTGAACCCAGGACAACTTATAG	1560
Db	1501		
QY	1561	CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCGTCTGATCTATGTTATCG	1620
Db	1561		
QY	1621	CCAACCTTTGAAAAACCTTTGAAAAAGCTGCTTTTCTGGTATTTAAAGTTTTAGAAATGCAA	1680
Db	1621		
QY	1681	GGAACTGTAATTTGGAGTTTCGCTCTTGTTATAATTTAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681		
QY	1741	GTAGAAAAGGAGGAATAATAATTTGGCTTAAATGAGAAATATCACCGGAATTTGAAAAA	1800
Db	1741		
QY	1801	ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA	1860
Db	1801		
QY	1861	TAAGCTGGTGGGAGAAAAATGAAAAACCTTATATTTAAAAATGACGGAACAGCCGGTATAAAGG	1920
Db	1861		
QY	1921	GACCACTTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC	1980
Db	1921		
QY	1981	TGTTTCAAAGGTCCTCAGCTTTGAAACGGCATGATGGCTGAGCAATCTGCTCATGATGA	2040
Db	1981		
QY	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
Db	2041		

Db	2041	GGCCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT	2100
QY	2101	CGAGCTGTATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTCGCCTA	2160
Db	2101		
QY	2161	TACGAATAGCTTACAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161		
QY	2221	CGATGTGGAATGCGAAAACTGGGAAAGAAACACTCCATTTAAAGATCCGCGCAGCTGTGA	2280
Db	2221		
QY	2281	TGATTTTTTAAACACGGAAAGCCCGAAGAGAACTTGCTTTTCCACCGCCACCTGGG	2340
Db	2281		
QY	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAAGTGGCTTTATTGATCTTTGGGAGAAG	2400
Db	2341		
QY	2401	CGCAGGCGGGAACAAGTGGTATGACATTTGCTTCTGCGTCCGCTCGATCAGGGAGGATAT	2460
Db	2401		
QY	2461	CGGGGAAGAACAGTATGTCAGCTATTTTGTACTTACTGGGATCAAGCTGATTCGGA	2520
Db	2461		
QY	2521	GAAAAATAAAATATATATTTACTGTGATGAATTTGTTTTAGTACTAGATGTGGCGCAACG	2580
Db	2521		
QY	2581	ATCCCGCGCAACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581		
QY	2641	CCGAGCCCAACGCAAGTATTTGGGCAAGGGTCTGCTGTTATTCGTGCAGGCGCAAGATTC	2700
Db	2641		
QY	2701	GGAAATACCAAGTACGAGAAGGCGCAGACGCTCTACGGGACCGACTTCATTTGCCGATA	2760
Db	2701		
QY	2761	AGGTGGATTATCTGGAACCAAGGCCACAGGCGGGTCAAATCAGGAATAAGGGCACATTG	2820
Db	2761		
QY	2821	CCCCGGCTGAGTCGGGGCAATCCGCCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA	2880
Db	2821		
QY	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCGAGGATGCCGCAACCATCG	2940
Db	2881		
QY	2941	CAAGCCGACCCGTCATCGCTGGCCCGCGGAAACCTTCCAGTCCGTCGGCTCGATGGTCC	3000
Db	2941		
QY	3001	AGCAAGCTACGGCAAGATCGAGCGGACAGCGTGCAACTGGCTCCCCCTGCCCCG	3060
Db	3001		
QY	3061	CGCCATCGGCGCGCTGGAGCGTTCCGTCGTCGAAACAGGAGGCGGAGGTTTGGCGA	3120
Db	3061		
QY	3121	AGTTCGATGACCACTCGACACGCGGAGAACTATGACGACCAAGAGCGGAAAAACCGCGCGG	3180
Db	3121		

Db	3121	AGTCGATGACCATCGACACGCGAGGAACACTATGACGACCAAGAACGGAATAACCGCCGGCG	3181
Qy	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCGTGTGCTGAAACACACGAAGC	3240
Db	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGCAGCGCGTGTGCTGAAACACACGAAGC	3240
Qy	3241	AGCAGATCAAGGAAATGCAGCTTTCCTTGTTCGATATTTGGCCGCTGCGGACACGATGC	3300
Db	3241	AGCAGATCAAGGAAATGCAGCTTTCCTTGTTCGATATTTGGCCGCTGCGGACACGATGC	3300
Qy	3301	GAGGGATCCAAACGACACGCGCGCTCTGCCCTGTTCACACGCGCACCAAGAAATCC	3360
Db	3301	GAGGGATCCAAACGACACGCGCGCTCTGCCCTGTTCACACGCGCACCAAGAAATCC	3360
Qy	3361	CGCGCAGGCGCTGCAAAAACAAGGTCAATTTTCAACGTCACAAAGGACGTTGAAGTCACTT	3420
Db	3361	CGCGCAGGCGCTGCAAAAACAAGGTCAATTTTCAACGTCACAAAGGACGTTGAAGTCACTT	3420
Qy	3421	ACACCGCGCTCGAGCTCGCGGCCGACGATCAAGAACTGGTGTGGCAGCAGTGTGGAGT	3480
Db	3421	ACACCGCGCTCGAGCTCGCGGCCGACGATCAAGAACTGGTGTGGCAGCAGTGTGGAGT	3480
Qy	3481	ACGCGAAGCGGACCCCTTATCGCGAGCGGATCACTTTCAGCTTCTACGACGTTTGCAGG	3540
Db	3481	ACGCGAAGCGGACCCCTTATCGCGAGCGGATCACTTTCAGCTTCTACGACGTTTGCAGG	3540
Qy	3541	ACCTGGGCTGTGCGATCAATGGCCGGTATTACACGAAGGCCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGGCTGTGCGATCAATGGCCGGTATTACACGAAGGCCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGGCGACGCGCGATGGGCTTCAACGTCGACCGCGTTGGGCACCTGGAAATCGGTGTGCG	3660
Db	3601	TACAGGCGACGCGCGATGGGCTTCAACGTCGACCGCGTTGGGCACCTGGAAATCGGTGTGCG	3660
Qy	3661	TGCTGCAACCGCTTCGGCGTCTCGACCGTGGCAAGAAAAAGTCCCGTGTGCAGGCTCTGA	3720
Db	3661	TGCTGCAACCGCTTCGGCGTCTCGACCGTGGCAAGAAAAAGTCCCGTGTGCAGGCTCTGA	3720
Qy	3721	TCGACGAGGAAATCGTCTGTGTTTCTGCGCACCACTACAGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATCGTCTGTGTTTCTGCGCACCACTACAGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAAGCTCTGCGCGACGCGCCGACGGAATGTTTCGACTATTTTCAGCTTCGACCGGG	3840
Db	3781	AGTACCGCAAGCTCTGCGCGACGCGCCGACGGAATGTTTCGACTATTTTCAGCTTCGACCGGG	3840
Qy	3841	AGCCGTACCCGCTCAAGCTGGAACACTTTCGCGCTCATGTGCGGATCGGAATTCACACCGCG	3900
Db	3841	AGCCGTACCCGCTCAAGCTGGAACACTTTCGCGCTCATGTGCGGATCGGAATTCACACCGCG	3900
Qy	3901	TGAAGAATGGCGGACGAGTCCGCGAAGCCTCGAAGAGTTCGCGAGGAGGAGCGGCTCG	3960
Db	3901	TGAAGAATGGCGGACGAGTCCGCGAAGCCTCGAAGAGTTCGCGAGGAGGAGCGGCTCG	3960
Qy	3961	TGGAAACGCGCTGGGTCAATGATCACTGTGTGATTCGAAACGCTAGGGCTTGTGGGGT	4020
Db	3961	TGGAAACGCGCTGGGTCAATGATGACCTGTGTGATTCGAAACGCTAGGGCTTGTGGGGT	4020
Qy	4021	CAGTTCGGGCTGGGGGTTTCAGCAGCAGCGCTTACTGGCATTTTCTAGGTGTGACGTCTT	4080
Db	4021	CAGTTCGGGCTGGGGGTTTCAGCAGCAGCGCTTACTGGCATTTTCTAGGTGTGACGTCTT	4080
Qy	4081	CTGATGGGCTGCGTGTATCGAGTGGTGATTTTGTGCGGAGCTGCGGTCGGGAGCGTGT	4140
Db	4081	CTGATGGGCTGCGTGTATCGAGTGGTGATTTTGTGCGGAGCTGCGGTCGGGAGCGTGT	4140
Qy	4141	GGCTGGGCTGGTGGCAGGATATTTGTGTGTGTAACAATTCGACGCTTAGACCACTTAATA	4200
Db	4141	GGCTGGGCTGGTGGCAGGATATTTGTGTGTGTAACAATTCGACGCTTAGACCACTTAATA	4200
Qy	4201	ACACATTCGGGACGCTTTTAAATGATCGGGGCTATTCGCCGGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTCGGGACGCTTTTAAATGATCGGGGCTATTCGCCGGGGGATATCCATAGGCCCG	4260

Qy	4261	ATCTAGTAACATTAATGACACCGCGCGGATATTTATCTAGTTTCGGCGCTATATTTTG	4320
Db	4261	ATCTAGTAACATTAATGACACCGCGCGGATATTTATCTAGTTTCGGCGCTATATTTTG	4320
Qy	4321	TTTTCTATCGCGTATTAAATGTATAATTCGGGACTCTAATCATATAAAACCCATCTCAT	4380
Db	4321	TTTTCTATCGCGTATTAAATGTATAATTCGGGACTCTAATCATATAAAACCCATCTCAT	4380
Qy	4381	AATAAGCTCATGCATTACATGTTTAATTATTACATGCTTAACGTAATTCACAGAAATTAT	4440
Db	4381	AATAAGCTCATGCATTACATGTTTAATTATTACATGCTTAACGTAATTCACAGAAATTAT	4440
Qy	4441	ATGATTAATCATCCAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
Db	4441	ATGATTAATCATCCAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
Qy	4501	TTTGAACGATCGTTCTGTCGAGCTATGGGCCGA	4533
Db	4501	TTTGAACGATCGTTCTGTCGAGCTATGGGCCGA	4533
RESULT 5			
AAF80277			
ID	AAF80277 standard; DNA; 5971 BP.		
XX	AAF80277;		
XX	29-JUN-2001 (first entry)		
XX	Nucleotide sequence of plasmid pMR1118.		
DE	Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;		
XX	P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.		
KW	Synthetic.		
OS	Synthetic.		
XX	Key		
FH	Location/Qualifiers		
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FT	CDS	655. .1263	
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FT	CDS	2604. .4098	
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FT	misc_feature	4106. .4271	
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FT	terminator	4272. .4559	
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FT	CDS	4560. .5556	
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FT		phosphotransferase and kanamycin resistance"	
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PN	XX		
XX	09-MAR-2001.		
PD	XX		
XX	03-SEP-1999;		
PF	99FR-00011112.		
XX	03-SEP-1999;		
PR	99FR-00011112.		

[illegible]

Db 1681 GGAACAGTGAATTTGGAGTTCGTCTTGTATTAATAGATCTTTGGGTAATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGCGTAAATAATGAGAAATATCACCGGAATTTGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGGAATAATAATGCGTAAATAATGAGAAATATCACCGGAATTTGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCGCTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGCTAAAGATACGGAAGGAATCTCTCTGCTAAGGTATA 1860  
Qy 1861 TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATACACGACAGCGCGGTATAAAGG 1920  
Db 1861 TAAGCTGGTGGGAGAAAAATGAAAAACCTATATTTAAAAATACACGACAGCGCGGTATAAAGG 1920  
Qy 1921 GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAAAGTGGC 1980  
Db 1921 GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAAAGTGGC 1980  
Qy 1981 TGTTCMAAGGTCTGCACTTTGAAACGGCATGATGCGTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCMAAGGTCTGCACTTTGAAACGGCATGATGCGTGGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GCGCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Db 2041 GCGCGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGAATTGTCCCTA 2160  
Db 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGAATTGTCCCTA 2160  
Qy 2161 TAGCAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATACCATCTGGC 2220  
Db 2161 TAGCAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATACCATCTGGC 2220  
Qy 2221 CGATGTGATTTGGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA 2280  
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Qy 2281 TGATTTTTTAAAGACGGAAAGCCCGAAGAGGAACCTTGTCTTTTCCACGCGCACTGGG 2340  
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Qy 2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCGCTCTCGGTCCGATCAGGGAGGATAT 2460  
Db 2401 CGGCAGGCGGACAAAGTGGTATGACATTTGCGCTCTCGGTCCGATCAGGGAGGATAT 2460  
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Qy 2581 ATGCCGCGCAACAGCAGGAGCGACCGACTTTCTTCGCGATCAAGTGTTTTGGCTCTCAGG 2640  
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Db 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCGCCGAGGATCGGAAACCATCG 2940  
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ID AAF80278 standard; DNA; 6016 BP.
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XX
XX 29-JUN-2001 (first entry)
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XX Nucleotide sequence of plasmid pMRT1119.
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XX (MORI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 94-96; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from pRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from pRK2 encoding the proteins P285 and P382.
XX
XX
XX CC The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX XX Sequence 6016 BP; 1512 A; 1525 C; 1669 G; 1310 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 4531.4; DB 4; Length 6016;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX DB 1 CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCCGCTCTATGGCCCTGCAAAACGCGCCAG 60
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XX DB 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGGCGGACTCAC 180
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XX DB 181 CCGGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTTGGCGGCGACGCTGAGCTGGC 240
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XX DB 241 CAGCCTCGAAATCGGCGAAACGCTGATTTTACGGAGTGTCCACAGATGATGGA 300
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XX DB 301 CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGGCGGACTTACTGACAGAT 360
XX
XX QY 361 GAGGGCGCGGATCTTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGGCGGACTTAT 420
XX DB 361 GAGGGCGCGGATCTTTGACACTTTGAGGGCGAGTGTGACAGATGAGGGGCGGACTTAT 420
XX
XX QY 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGACTTTCGAGGGTTCGCGCGGT 480
XX DB 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGACTTTCGAGGGTTCGCGCGGT 480
XX
XX QY 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTCTTTTAAACCAATATTTATAACCTTG 540
XX DB 481 TTTTCGGCCACCGCTAACCTGTCTTTTAACTCTTTTAAACCAATATTTATAACCTTG 540
XX
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XX DB 541 TTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGGCGACCGCGAGGGGGTGCCTCCC 600
XX
XX QY 601 CTTCTCGAACCTCCCGGAAAGTATGCGGTGTGAATACCGCACAGATCGGTAAAGGAGA 660
XX DB 601 CTTCTCGAACCTCCCGGAAAGTATGCGGTGTGAATACCGCACAGATCGGTAAAGGAGA 660
XX
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XX
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XX DB 781 GGGGATHAACCGAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAA 840
XX
XX QY 841 AAGCGCGCTGTGCTGGGCTTTTCCATAGGCTCGGCCCTTCCAGAGCTACCAAAAT 900
XX DB 841 AAGCGCGCTGTGCTGGGCTTTTCCATAGGCTCGGCCCTTCCAGAGCTACCAAAAT 900
XX
XX QY 901 CGACGCTCAAGTCAGAGGTGGCGAAACCGGACAGGACTATAAGATACCGAGGCTTTCCC 960
XX DB 901 CGACGCTCAAGTCAGAGGTGGCGAAACCGGACAGGACTATAAGATACCGAGGCTTTCCC 960

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Db 901 CGAGCCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCC 960  
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Db 961 CCTGGAAGCTCCCTCGTCGCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC 1020  
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Db 1021 GCCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT 1080  
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Db |||||  
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RESULT 8  
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ID AAF80281 standard; DNA; 6017 BP.  
XX  
AC AAF80281;  
XX AC  
DT 29-JUN-2001 (first entry)  
XX  
DE Nucleotide sequence of plasmid pMRT1155.  
XX  
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT rep\_origin 1..654  
FT /tag= a  
FT /note= "ori RK2"  
FT rep\_origin 655..1263  
FT /tag= b  
FT /note= "ori Cole1"  
FT CDS 1264..2603  
FT /tag= c  
FT /note= "NPT III gene coding for neomycin  
FT phosphotransferase and kanamycin resistance"  
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FT promoter 5557..5771  
FT /tag= h  
FT /note= "nopaline synthetase promoter"  
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FT /tag= i  
FT /note= "T-DNA right border"  
XX  
PN FR2798139-A1.  
XX

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XX		DB		
PF	03-SEP-1999; 99FR-00011112.		TTTTTAACAGGGCTCGCCCTGTGCGCGTACCGCGCACCGCGAAGGGGGTGCSCCCC	600
XX				
PR	03-SEP-1999; 99FR-00011112.	QY	CTTCTCGAAACCTTCGCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGCTAAGAGA	660
XX		DB		
PA	(MERI-) MERISTEM THERAPEUTICS SA.		CTTCTCGAAACCTTCGCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGCTAAGAGA	660
XX				
P1	Gruber V, Comeau D;	QY	AAATACCGCATCAGGCGCTCTTCGCGTCTCTCGCTCACTGACTCGCTCGCTCGCTCGTT	720
XX		DB		
DR	WPI; 2001-259847/27.		AAATACCGCATCAGGCGCTCTTCGCGTCTCTCGCTCACTGACTCGCTCGCTCGCTCGTT	720
XX				
PT	New vector free from non-essential elements, useful for transforming	QY	CGSCTCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGATCA	780
XX	cells for protein production and for preparing transgenic plants.	DB		
PS	Claim 20; Page 104-106; 180pp; French.		CGSCTCGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGATCA	780
XX		QY	GGGGATAACGCGAGGAAAGAACATGTGAGCAAAAGGCGCAGAAAGGCCAGGAACCGTAAA	840
CC	The specification describes a synthetic vector containing only those	DB		
CC	elements essential for its functionality and transgenesis of a cell		GGGGATAACGCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCGTAAA	840
CC	(especially a plant cell). The vector consists of at most one origin of	QY	AAGGCGCGCTTGTCTGCGCTTTTTCATAGCTCCGCGCCCTCGACGAGCATCAAAAAT	900
CC	replication (ori), at most one sequence encoding a selection agent and a	DB		
CC	trfA locus encoding a protein that increases the level of plasmid		AAGGCGCGCTTGTCTGCGCTTTTTCATAGCTCCGCGCCCTCGACGAGCATCAAAAAT	900
CC	replication. The vector particularly contains an RK2 ori, especially oriv	DB		
CC	from PRK2 of Escherichia coli with a broad host range, an antibiotic	QY	CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGAGACTATAAAGATACACAGGCGTTTCCC	960
CC	resistance gene (especially nptII conferring resistance to kanamycin in	DB		
CC	bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.		CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGAGACTATAAAGATACACAGGCGTTTCCC	960
CC	The vectors are used to prepare transgenic plants and transformed host	QY	CTTGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTGTC	1020
CC	cells for production of a heterologous proteins, e.g. insulin,	DB		
CC	interferon, lipase, blood proteins and anti-inflammatory agents. The		CTTGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTGTC	1020
CC	present sequence represents a plasmid of the invention	QY	GCCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGATAGTATCTCAGT	1080
XX		DB		
SQ	Sequence 6017 BP; 1512 A; 1525 C; 1669 G; 1311 T; 0 U; 0 Other;		GCCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGATAGTATCTCAGT	1080
	Query Match 94.3%; Score 4531.4; DB 4; Length 6017;	QY	TCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGTGCACGAAACCCCGCTTCAGCCCGAC	1140
	Best Local Similarity 100.0%; Pred. No. 0;	DB		
	Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		TCGGTGTAGTTCGTTCCGCTCCAAAGCTGGGCTGTGTGCACGAAACCCCGCTTCAGCCCGAC	1140
QY	1 CCGGGCTGGTGTGCTCGCGCTGGGCTGGCGCGCTATGCTGCTGCAAGCGCGAG 60	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	61 AAACGCGCTGCAAGCGCGTGTGCAGACACCGCGCGCGCGGCTTGTGGATACCTCGCGG 120	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	121 AAACCTTGGCCCTCACTGCAGATGAGGGCGGAGCTTGACATTTGAGGGCGGACTCAC 180	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	181 CCGCGCGCGCTTGCAGATGAGGGCGAGGCTCGATTTTCGCGCGCGACGCTGGAGCTGGC 240	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	241 CAGCCTCGAAATCGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGGGA 300	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	301 CAAGCCTGGGGATAAGTGCCCTCGGTTATGACACTTTGAGGGCGGCGACTACTGACAGAT 360	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	361 GAGGGCGCGCATCTTGACACTTTGAGGGCGAGAGTGTGACAGATGAGGGCGGCGACTTAT 420	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCGCGT 480	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
QY	481 TTTTGGCGCACCGGTAACTGTCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTT 540	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200
DB		DB		
	481 TTTTGGCGCACCGGTAACTGTCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTT 540	QY	CGCTGTAGTTCGTTCCGCTTAACCTATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCG	1200







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Qy 181 CCGCGCGGGCTTGACAGATGAGGGGAGGCTCGAATTCGGCGCGGAGCACTGAGCTGGC 240  
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Qy 301 CAAAGCTGGGGAATAAGTGCCTCGGTATTTGACACTTGAGGGGCGGACTTACTGACAGAT 360  
Db 301 CAAAGCTGGGGAATAAGTGCCTCGGTATTTGACACTTGAGGGGCGGACTTACTGACAGAT 360  
Qy 361 GAGGGCGCGATCCTTGACACTTTGAGGGGAGAGTGTGTGACAGATGAGGGGCGGACTTAT 420  
Db 361 GAGGGCGCGATCCTTGACACTTTGAGGGGAGAGTGTGTGACAGATGAGGGGCGGACTTAT 420  
Qy 421 TGACATTTGAGGGGCTGTCCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGT 480  
Db 421 TGACATTTGAGGGGCTGTCCACAGGCAAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGT 480  
Qy 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG 540  
Db 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG 540  
Qy 541 TTTTAAACAGGGCTGCGCCTGTGCGCGTGAACGCGCAACGCGAAGGGGGGTGCCCCC 600  
Db 541 TTTTAAACAGGGCTGCGCCTGTGCGCGTGAACGCGCAACGCGAAGGGGGGTGCCCCC 600  
Qy 601 CTCTCGAACCCCTCCGGAAAGTATCGGCTGTGAAATACCGACAGATCGTAAGGAGA 660  
Db 601 CTCTCGAACCCCTCCGGAAAGTATCGGCTGTGAAATACCGACAGATCGTAAGGAGA 660  
Qy 661 AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGTT 720  
Db 661 AAATACCGCATCAGGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGTT 720  
Qy 721 CCGCTGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACCGATCA 780  
Db 721 CCGCTGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACCGATCA 780  
Qy 781 GGGGATAACCGAAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA 840  
Db 781 GGGGATAACCGAAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACCGTAAA 840  
Qy 841 AAGCCCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAAT 900  
Db 841 AAGCCCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAAT 900  
Qy 901 CGAGCTCAAGTCAAGAGTGGCGAAACCCGACAGGACTATAAGATACGAGCGGTTTCCC 960  
Db 901 CGAGCTCAAGTCAAGAGTGGCGAAACCCGACAGGACTATAAGATACGAGCGGTTTCCC 960  
Qy 961 CTTGGAAGCTCCCTCGGCTCTCTGTTCCGACCTCGCGCTTACCGGATCCTGTCC 1020  
Db 961 CTTGGAAGCTCCCTCGGCTCTCTGTTCCGACCTCGCGCTTACCGGATCCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT 1080  
Qy 1081 TCGGTGATAGTTCGTTCCAGCTGGCTGTGTGACGAAACCCCGGTTTCAGCCCGAC 1140  
Db 1081 TCGGTGATAGTTCGTTCCAGCTGGCTGTGTGACGAAACCCCGGTTTCAGCCCGAC 1140  
Qy 1141 CGCTGCGCTTATCCGGTAACCTATCTGTTCCGACCTCCAAACCGGTAAAGACGACTTATCG 1200  
Db 1141 CGCTGCGCTTATCCGGTAACCTATCTGTTCCGACCTCCAAACCGGTAAAGACGACTTATCG 1200  
Qy 1201 CCACTGGCAGCAGCTTCTACCATAAATCCGCGATAAACCCAGCAACCATTTGAGGTGAT 1260  
Db 1201 CCACTGGCAGCAGCTTCTACCATAAATCCGCGATAAACCCAGCAACCATTTGAGGTGAT 1260

Qy 1261 AGGTAAGATTATACCGAGGTATGAAAAAGAGAAATTTGACCTTTTACAGAAATTTACTCTATGA 1320  
Db 1261 AGGTAAGATTATACCGAGGTATGAAAAAGAGAAATTTGACCTTTTACAGAAATTTACTCTATGA 1320  
Qy 1321 AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGAGGCAGATTG 1380  
Db 1321 AGCGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGATGAGAGGCAGATTG 1380  
Qy 1381 CTTTGAATATATTTGACAACTACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG 1440  
Db 1381 CTTTGAATATATTTGACAACTACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG 1440  
Qy 1441 TATGTAAGATTTTACGGGGCAAGGCATAGGCAGCGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAGATTTTACGGGGCAAGGCATAGGCAGCGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAAACTTTGAAAGCTGTTTCTGGTATTTTAAAGTTTTAGAAATGCAA 1560  
Db 1501 GGGCAAGCATAAAACTTTGAAAGCTGTTTCTGGTATTTTAAAGTTTTAGAAATGCAA 1560  
Qy 1561 CTTTGAATTTTACCAAAATTTGGTTCAAAATCGGCTCGCTGATCTATGTTATACG 1620  
Db 1561 CTTTGAATTTTACCAAAATTTGGTTCAAAATCGGCTCGCTGATCTATGTTATACG 1620  
Qy 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTCTGGTATTTTAAAGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAAAACAATTTGAAAAAGCTGTTTCTGGTATTTTAAAGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGGAGTTTCGCTTGTATATAATAGTCTTCTGGGTTTCTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTTCGCTTGTATATAATAGTCTTCTGGGTTTCTTAAATACT 1740  
Qy 1741 GTAGAAAAAGGAAAGAAATATAAATGCTTAAATGAGAATATCACCGAAATTTGAAAAA 1800  
Db 1741 GTAGAAAAAGGAAAGAAATATAAATGCTTAAATGAGAATATCACCGAAATTTGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCTGTAAGAAATACGGAAGAAATGCTCTCTCAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCTGTAAGAAATACGGAAGAAATGCTCTCTCAAGGTATA 1860  
Qy 1861 TAAAGCTGGTGGGAGAAAACTTATATTTAAAAATGACGAGCAGCGCGTATAAAGG 1920  
Db 1861 TAAAGCTGGTGGGAGAAAACTTATATTTAAAAATGACGAGCAGCGCGTATAAAGG 1920  
Qy 1921 GACCACTATGATGTGGACGGGAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Db 1921 GACCACTATGATGTGGACGGGAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Qy 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCAGATGCGCTCTTTGCTCGGAAAGATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCAGATGCGCTCTTTGCTCGGAAAGATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Db 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Qy 2161 TACGAATAGCTTACAGACGCGCTTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTACAGACGCGCTTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy 2221 CGATGTGATTTGCGAAACCTGGGAAAGAGACATCTCCATTTTAAAGATCCGCGGAGCTGTA 2280  
Db 2221 CGATGTGATTTGCGAAACCTGGGAAAGAGACATCTCCATTTTAAAGATCCGCGGAGCTGTA 2280  
Qy 2281 TGATTTTTTAAAGCAGAAAGCCGGAAGAGAACTTTGCTTTTCCACCGGACCTGGG 2340  
Db 2281 TGATTTTTTAAAGCAGAAAGCCGGAAGAGAACTTTGCTTTTCCACCGGACCTGGG 2340



QY	2341	AGACAGCAACATCTTTGTGAAAGATGCGAAGTAAGTGGCTTTATTGATCTTTGGGAGAAG	2400
DB	2341	AGACAGCAACATCTTTGTGAAAGATGCGAAGTAAGTGGCTTTATTGATCTTTGGGAGAAG	2400
QY	2401	CGGCAGGCGGACAAAGTGGTATGACATTTGCCCTTCGCTCGCTCGGTCGATCAGGGAGGATAT	2460
DB	2401	CGGCAGGCGGACAAAGTGGTATGACATTTGCCCTTCGCTCGGTCGATCAGGGAGGATAT	2460
QY	2461	CGGGGAAGAAACAGTATGTCGAGCTATTTTGTGACTTACTGCGGATCAAGGCTGATTGGGA	2520
DB	2461	CGGGGAAGAAACAGTATGTCGAGCTATTTTGTGACTTACTGCGGATCAAGGCTGATTGGGA	2520
QY	2521	GAATAATAAATAATTAATTTACTTCTGAGTAAATTTGTTTAGTACTAGATGTGGCGCAACG	2580
DB	2521	GAATAATAAATAATTAATTTACTTCTGAGTAAATTTGTTTAGTACTAGATGTGGCGCAACG	2580
QY	2581	ATGCCGGCGACAACGAGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
DB	2581	ATGCCGGCGACAACGAGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
QY	2641	CCGAGGGCCACCGCAAGTATTTGGCGAAGGGTCCGCTGGTATTCGTGCAGGGCAAGATTTC	2700
DB	2641	CCGAGGGCCACCGCAAGTATTTGGCGAAGGGTCCGCTGGTATTCGTGCAGGGCAAGATTTC	2700
QY	2701	GGAAATCAACAGTACGAGAAGACCGCCAGACCGTCTACGGGACCGACTTCATTGCCGATA	2760
DB	2701	GGAAATCAACAGTACGAGAAGACCGCCAGACCGTCTACGGGACCGACTTCATTGCCGATA	2760
QY	2761	AGGTGGATTATCTCGACACCAAGGACACGCGGGTCAAAATCAGGANTAGGGCACAATTG	2820
DB	2761	AGGTGGATTATCTCGACACCAAGGACACGCGGGTCAAAATCAGGANTAGGGCACAATTG	2820
QY	2821	CCCCGGGCTGAGTCCGGGCAATCCCGCAAGAGGGTGAATGAATCGGACCGTTTGACCGGA	2880
DB	2821	CCCCGGGCTGAGTCCGGGCAATCCCGCAAGAGGGTGAATGAATCGGACCGTTTGACCGGA	2880
QY	2881	AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCCGCGAGGATGCGCGAAACCATCG	2940
DB	2881	AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCCGCGAGGATGCGCGAAACCATCG	2940
QY	2941	CAAGCCGACCGTCAATCGGTGCGCCCGCGAACCCTTCCAGTCCGCTCGGCTCGATGGTCC	3000
DB	2941	CAAGCCGACCGTCAATCGGTGCGCCCGCGAACCCTTCCAGTCCGCTCGGCTCGATGGTCC	3000
QY	3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTGCAACTGGTCCCGCTGCCCTGCCCG	3060
DB	3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACAGCGTGCAACTGGTCCCGCTGCCCTGCCCG	3060
QY	3061	CGCCATCGGCGCGCTGGAGCGTTTCGCTCGAACAGGAGGCGGCAAGTGTGGCGA	3120
DB	3061	CGCCATCGGCGCGCTGGAGCGTTTCGCTCGAACAGGAGGCGGCAAGTGTGGCGA	3120
QY	3121	AGTCGATGACCATCGACACGGGAGGAATATGACCGACAGAGACGGAATAACCGCGCGG	3180
DB	3121	AGTCGATGACCATCGACACGGGAGGAATATGACCGACAGAGACGGAATAACCGCGCGG	3180
QY	3181	AGGACCTGGCAAAAACAGTCAAGGAGGCCAAGCAGGCGGTTGCTGTAAACACACGAAGC	3240
DB	3181	AGGACCTGGCAAAAACAGTCAAGGAGGCCAAGCAGGCGGTTGCTGTAAACACACGAAGC	3240
QY	3241	AGCAGATCAAGGAAATCAGCTTTCTTGTTCGATATTGCGCGCTGCGCCGCGACACGATGC	3300
DB	3241	AGCAGATCAAGGAAATCAGCTTTCTTGTTCGATATTGCGCGCTGCGCCGCGACACGATGC	3300
QY	3301	GAGCGATGCCAAACGACACGGCCGCTCTGCCCTGTTCACACGGCGCAACAGAAATTC	3360
DB	3301	GAGCGATGCCAAACGACACGGCCGCTCTGCCCTGTTCACACGGCGCAACAGAAATTC	3360
QY	3361	CGCGCAGGCGCTCGAAAACAAAGTCAATTTTCCAGCTCAACAGGACGTTGAAGTCACTT	3420
DB	3361	CGCGCAGGCGCTCGAAAACAAAGTCAATTTTCCAGCTCAACAGGACGTTGAAGTCACTT	3420
QY	3421	ACACCGGCTGAGCTCGGGGCGACGATGACGAACTGGTGTGGCAGCAGGCTGTGGAGT	3480

3421		ACACCGCGTCGAGCTCGCGGCGACGATGACGAACCTGGTGTGCGACGAGTGTGGAGT	3480
3481		ACGCGAAGCGCACCCCTATCCGGCGAGCGCGATCACCTTACGTTCTACGAGCTTTGCCAGG	3540
3481		ACGCGAAGCGCACCCCTATCCGGCGAGCGGATCACCTTACGTTCTACGAGCTTTGCCAGG	3540
3541		ACCTGGGCTGGTCCGATCAATGGCCGGTATTACACGAAGGCGAGGAATGCTGTGCGGCC	3600
3541		ACCTGGGCTGGTCCGATCAATGGCCGGTATTACACGAAGGCGAGGAATGCTGTGCGGCC	3600
3601		TACAGGCGACGGCGATGGGCTTACGTCGACCGCGTTGGGCACTTGGGAATCGGTGTCG	3660
3601		TACAGGCGACGGCGATGGGCTTACGTCGACCGCGTTGGGCACTTGGGAATCGGTGTCG	3660
3661		TGCTGCACCGCTTCCGGCTCTCGACCGTGGCAAGAAACGTCGCCGTTGCCAGGTCCTGA	3720
3661		TGCTGCACCGCTTCCGGCTCTCGACCGTGGCAAGAAACGTCGCCGTTGCCAGGTCCTGA	3720
3721		TCGACGAGGAAATCGTCGTGCTGTTGCTGGCGACCACTACACGAAATTCATATGGAGA	3780
3721		TCGACGAGGAAATCGTCGTGCTGTTGCTGGCGACCACTACACGAAATTCATATGGAGA	3780
3781		AGTACGCGAAGCTGTCCGCGACGGCCCGACGGATGTTCGACTATTTACGCTCGCACCGGG	3840
3781		AGTACGCGAAGCTGTCCGCGACGGCCCGACGGATGTTCGACTATTTACGCTCGCACCGGG	3840
3841		AGCGGTACCCGCTCAAGCTTGGAAACCTTCGCGCTCATGTGCGGATCGGATTCACACCGCG	3900
3841		AGCGGTACCCGCTCAAGCTTGGAAACCTTCGCGCTCATGTGCGGATCGGATTCACACCGCG	3900
3901		TGAAGAAGTGGCGGACGAGTTCGCGAAGCCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
3901		TGAAGAAGTGGCGGACGAGTTCGCGAAGCCTTCGCAAGAGTTGCGAGGCGAGCGGCTGG	3960
3961		TGAAACAACGCTGGGTCAATGATGACTGGTGCAITTCGAAAACGCTAGGGCTTTGTGGGGT	4020
3961		TGAAACAACGCTGGGTCAATGATGACTGGTGCAITTCGAAAACGCTAGGGCTTTGTGGGGT	4020
4021		CAGTTCGGGTGGGGTTCAGACGCCAGCGCTTTACTGCGATTTCTAGGCTTCACGCTTT	4080
4021		CAGTTCGGGTGGGGTTCAGACGCCAGCGCTTTACTGCGATTTCTAGGCTTCACGCTTT	4080
4081		CTGATGGGCTGCCGTATCGAGTGGTGATTTTGTGCGGAGCTGCGGTCGGGAGCTGTT	4140
4081		CTGATGGGCTGCCGTATCGAGTGGTGATTTTGTGCGGAGCTGCGGTCGGGAGCTGTT	4140
4141		GGCTGGCTGGTGCAGGATATATTGGTGGTGAACAAATTTAGCTTTAGACAACTTAATA	4200
4141		GGCTGGCTGGTGCAGGATATATTGGTGGTGAACAAATTTAGCTTTAGACAACTTAATA	4200
4201		ACACATTCGGGAGCTTTTAATGCTACTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
4201		ACACATTCGGGAGCTTTTAATGCTACTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
4261		ATCTAGTAACATAATGACACCGCGCGATTAATTTATCTAGTTTCGGCGCTATATTTTG	4320
4261		ATCTAGTAACATAATGACACCGCGCGATTAATTTATCTAGTTTCGGCGCTATATTTTG	4320
4321		TTTTTCTATCCGCTTTAAATGATATAATTCGGGACTCTAATCATAAAAACCCCATCTCAT	4380
4321		TTTTTCTATCCGCTTTAAATGATATAATTCGGGACTCTAATCATAAAAACCCCATCTCAT	4380
4381		AATAACGCTCATGCAATGATGTTAATTTATACATGCTTAAACGTAATTCACAGAAATTT	4440
4381		AATAACGCTCATGCAATGATGTTAATTTATACATGCTTAAACGTAATTCACAGAAATTT	4440
4441		ATGATAATCATCGAAGACCGGCAACAGGATTCAAATCTTTAAGAAACCTTTATTGCCAAATG	4500
4441		ATGATAATCATCGAAGACCGGCAACAGGATTCAAATCTTTAAGAAACCTTTATTGCCAAATG	4500
4501		TTTGAACGATCGTTCGTGAGCTATGGGCCGA 4533	

Db 4501 TTTGAACGATCGTTCTCGAGCTATGGGCCAA 4533

RESULT 10

AAF80282

ID AAF80282 standard; DNA; 6767 BP.

XX AAF80282;

AC AAF80282;

XX 29-JUN-2001 (first entry)

DT

XX Nucleotide sequence of plasmid pMRT1175.

DE

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;

KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.

KW

XX Synthetic.

OS

XX

FH Key Location/Qualifiers

FT rep\_origin 1..654

FT /\*tag= a

FT /note= "ori RK2"

FT

FT rep\_origin 655..1263

FT /\*tag= b

FT /note= "ori Cole1"

FT CDS 1264..2603

FT /\*tag= c

FT /note= "NPT III gene coding for neomycin

FT phosphotransferase and kanamycin resistance"

FT CDS 2604..4098

FT /\*tag= d

FT /note= "trfA locus from RK2 coding for two proteins P285

FT and P382 enabling an increase in the replication rate"

FT misc\_feature 4106..4271

FT /\*tag= e

FT /note= "T-DNA left border"

FT terminator 4272..4559

FT /\*tag= f

FT /note= "nopaline synthetase terminator"

FT CDS 4559..5556

FT /\*tag= g

FT /note= "NPT III gene coding for neomycin

FT phosphotransferase and kanamycin resistance"

FT promoter 5557..5771

FT /\*tag= h

FT /note= "nopaline synthetase promoter"

FT polyA\_signal 5830..6560

FT /\*tag= i

FT /note= "polyA from 35S ribosome"

FT misc\_feature 6587..6760

FT /\*tag= j

FT /note= "T-DNA right border"

XX

PN FR2798139-A1.

XX

XX 09-MAR-2001.

XX

XX 03-SEP-1999; 99FR-00011112.

XX

XX 03-SEP-1999; 99FR-00011112.

XX (MERI-) MERISTEM THERAPEUTICS SA.

XX

XX Gruber V, Comeau D;

XX

XX WPI: 2001-259847/27.

XX

XX New vector free from non-essential elements, useful for transforming

FT cells for protein production and for preparing transgenic plants.

XX

XX Claim 20; Page 108-110; 180pp; French.

PS

XX The specification describes a synthetic vector containing only those

CC

CC elements essential for its functionality and transgenesis of a cell

CC (especially a plant cell). The vector consists of at most one origin of

CC replication (ori), at most one sequence encoding a selection agent and a

CC trfA locus encoding a protein that increases the level of plasmid

CC replication. The vector particularly contains an RK2 ori, especially oriv

CC from PRK2 of Escherichia coli with a broad host range, an antibiotic

CC resistance gene (especially nptIII conferring resistance to kanamycin in

CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.

CC The vectors are used to prepare transgenic plants and transformed host

CC cells for production of a heterologous proteins, e.g. insulin,

CC interferon, lipase, blood proteins and anti-inflammatory agents. The

CC present sequence represents a plasmid of the invention

XX

SQ Sequence 6767 BP; 1762 A; 1675 C; 1821 G; 1509 T; 0 U; 0 Other;

Query Match 94.3%; Score 4531.4; DB 4; Length 6767;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTTGCCCTCGCGCTGGCTGGCGCGCTGTATGCCCTGCAACGCCCCAG 60

DB |||||

QY 1 CCGGGCTGGTTGCCCTCGCGCTGGCGCGCTGTATGCCCTGCAACGCCCCAG 60

DB |||||

QY 61 AAGCGCGTGAAGCGCTGTGGAGACACCGCGCGCGCGCTGTGGATACCTCGCG 120

DB |||||

QY 61 AAGCGCGTGAAGCGCTGTGGAGACACCGCGCGCGCGCTGTGGATACCTCGCG 120

DB |||||

QY 121 AAGCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTC 180

DB |||||

QY 121 AAGCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTC 180

DB |||||

QY 181 CCGGGCGCGCTGTGACAGATGAGGGCGGCTGATTTCCGCGCGGCGGCTGAGTGGG 240

DB |||||

QY 181 CCGGGCGCGCTGTGACAGATGAGGGCGGCTGATTTCCGCGCGGCGGCTGAGTGGG 240

DB |||||

QY 241 CAGCCTCGCAAAATCGCGGAAACGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300

DB |||||

QY 241 CAGCCTCGCAAAATCGCGGAAACGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300

DB |||||

QY 301 CAGCCTCGGGGATAAGTGGCTTGTGACACTTGAAGGGCGGCGGCTGACAGAT 360

DB |||||

QY 301 CAGCCTCGGGGATAAGTGGCTTGTGACACTTGAAGGGCGGCGGCTGACAGAT 360

DB |||||

QY 361 GAGGGCGGCTGCTTGAACACTTGAAGGGCGGCTGACAGATGAGGGCGGCGGCTGAT 420

DB |||||

QY 361 GAGGGCGGCTGCTTGAACACTTGAAGGGCGGCTGACAGATGAGGGCGGCGGCTGAT 420

DB |||||

QY 421 TGACATTTGAGGGGCTGTCACAGGAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGT 480

DB |||||

QY 421 TGACATTTGAGGGGCTGTCACAGGAGAAATCCAGCAATTTGCAAGGGTTTCGCGCGT 480

DB |||||

QY 481 TTTTCGCGCAACCGCTAACCTGCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540

DB |||||

QY 481 TTTTCGCGCAACCGCTAACCTGCTTTTAACTGCTTTTAAACCAATATTTTAAACCTTG 540

DB |||||

QY 541 TTTTAAACCGAGGCTGCGCGCTGCGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGG 600

DB |||||

QY 541 TTTTAAACCGAGGCTGCGCGCTGCGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGG 600

DB |||||

QY 601 CTTCTCGAACCTTCCCGGAAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGAGA 660

DB |||||

QY 601 CTTCTCGAACCTTCCCGGAAAGGTATGCGGTGTGAATACCGCACAGATCGTAAGAGA 660

DB |||||

QY 661 AAATACCGATCAGGGCTCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCT 720

DB |||||

QY 661 AAATACCGATCAGGGCTCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCT 720

DB |||||

QY 721 CGGCTCGGCGAGCGGTATCAGCTCACTAAAGCGGTATACGTTTATCCACAGATCA 780

DB |||||

QY 721 CGGCTCGGCGAGCGGTATCAGCTCACTAAAGCGGTATACGTTTATCCACAGATCA 780

DB |||||

QY 781 GGGGATAACCGAGGAAAGATGTGAGCAAAAGGCGGCGGCGGCGGCGGCGGCGGCGG 840

DB |||||

Db 781 GGGGATAA CCGCAGGAAGAA CATGTGAGCAAAAAGGCCAGAAAGCCGAGTAA 840  
Qy 841 AAGCCGCGTGTGCTGGCGTTTTTCCATAGCTCCGCCCTCCCTGACGAGCATCACAAAAAT 900  
Db 841 AAGCCGCGTGTGCTGGCGTTTTTCCATAGCTCCGCCCTCCCTGACGAGCATCACAAAAAT 900  
Qy 901 CGACGCTCAAGTCAGAGGTGGCAAAACCGACAGGACTATAAAGATACACAGGCGTTTCCC 960  
Db 901 CGACGCTCAAGTCAGAGGTGGCAAAACCGACAGGACTATAAAGATACACAGGCGTTTCCC 960  
Qy 961 CTTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGATACCTGTCC 1020  
Db 961 CTTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGATACCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 1080  
Db 1021 GCCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGT 1080  
Qy 1081 TCGGTGTAGTGTGCTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC 1140  
Db 1081 TCGGTGTAGTGTGCTCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC 1140  
Qy 1141 CGCTGGCGCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAGACACGACTTATCG 1200  
Db 1141 CGCTGGCGCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAGACACGACTTATCG 1200  
Qy 1201 CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAACCAATTTGAGGTGAT 1260  
Db 1201 CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCAGCGAACCAATTTGAGGTGAT 1260  
Qy 1261 AGTAAAGATTATCCGAGGTATGA AAA CGAGAAATTCGACTTTTACAGAAATTTACTCTATGA 1320  
Db 1261 AGTAAAGATTATCCGAGGTATGA AAA CGAGAAATTCGACTTTTACAGAAATTTACTCTATGA 1320  
Qy 1321 AGCGGCATATTTAAAAGCTTACCAACGAGAGGATGAAGAGTACGAGGACGATTTG 1380  
Db 1321 AGCGGCATATTTAAAAGCTTACCAACGAGAGGATGAAGAGTACGAGGACGATTTG 1380  
Qy 1381 CTTGTAATATATTGACAACTACTGATAAGATAATACATCTTTTATAGAAATATCGCCG 1440  
Db 1381 CTTGTAATATATTGACAACTACTGATAAGATAATACATCTTTTATAGAAATATCGCCG 1440  
Qy 1441 TATGTAAGGATTTACGGGGCAAGGATAGGACGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAGGATTTACGGGGCAAGGATAGGACGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAAATACCTTATAG 1560  
Db 1501 GGGCAAGCATAAAACTTGCATGGACTAATGCTTGAACCCAGGACAAATACCTTATAG 1560  
Qy 1561 CTTGTAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATATCTATGTTATACG 1620  
Db 1561 CTTGTAATTTTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATATCTATGTTATACG 1620  
Qy 1621 CCAACTTTGAAAAACA ACTTTGAAAAAGCTGTTTTCTGTTATTTAAGGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAAAACA ACTTTGAAAAAGCTGTTTTCTGTTATTTAAGGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACTGTAATGGAGTTGCTGTTGTTATTAATAGCTTCTGGGGTATCTTTAAATACT 1740  
Db 1681 GGAACTGTAATGGAGTTGCTGTTGTTATTAATAGCTTCTGGGGTATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGCTTAAATGAGAATATACCGGAATTTGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAATGCTTAAATGAGAATATACCGGAATTTGAAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGGGTAAAAGATACGGAAGGAATGTCCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGGGTAAAAGATACGGAAGGAATGTCCTCTGCTAAGGTATA 1860  
Qy 1861 TAACTGTGGGAGAAAATGAAAA CCTATATTTAAAAATGACGGACAGCCGGTATAAAGG 1920  
Db 1861 TAACTGTGGGAGAAAATGAAAA CCTATATTTAAAAATGACGGACAGCCGGTATAAAGG 1920

Qy 1921 GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Qy 1981 TGTTCCAAAGTCTGTCACATTTTGAACGGGATGATGCTGAGGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCCAAAGTCTGTCACATTTTGAACGGGATGATGCTGAGGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCAGATGCGCTCTTTGCTCGGAAGATGATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCAGATGCGCTCTTTGCTCGGAAGATGATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTGTCCCTA 2160  
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Qy 2221 CGATGTGGATTGCGAAAACTGGGAAAGACACACTCCATTTAAAGATCCCGCGGAGTGTGA 2280  
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Qy 2401 CGGCGGGCGGACAGTGGTATGACATTCGCTTCTGCGTCCGTCGATCAGGAGGATAT 2460  
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Qy 2521 GAAAATAAATAATATATTTTACTGATGAATTTGTTTTAGTACCTAGATGTGGCGCAACG 2580  
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Qy 2581 ATGCCGGCGACAAAGCAGGAGCGCACCGACTTCTTCGCAATCAAGTGTTTGGCTCTCAGG 2640  
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Qy 2641 CCGAGGCCCAACGGCAAGTATTTTGGGCAAGGGTCTGCTGATTTTCTGTCAGGGCAAGATTC 2700  
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Qy 2701 GGAATACCAAGTACGAGAAAGGACGGCTCTACGGGACCGACTTCTATTTGCCGATA 2760  
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Qy 2881 AGGCATACAGGCAAGAACTGATCGACGGGGTTTTTCCGCCAGGATCCGAAACCATCG 2940  
Db 2881 AGGCATACAGGCAAGAACTGATCGACGGGGTTTTTCCGCCAGGATCCGAAACCATCG 2940  
Qy 2941 CAAAGCGCACCGTCTATGCTGCGCCCGCGGAAACCTTCCAGTCCGTCGCTCGATGGTCC 3000  
Db 2941 CAAAGCGCACCGTCTATGCTGCGCCCGCGGAAACCTTCCAGTCCGTCGCTCGATGGTCC 3000





1441	Db	TATGTAAGGATTCTCAGGGGCAAGGCATAGCGACGGCGCTTATCAATATATCTATAGAAAT	1500
1501	Qy	GGGCAAGCATAAAACTTCGATCGGACTAATGCTTGAAACCCAGGACAAATAACCTTATAG	1560
1501	Db	GGGCAAGCATAAAACTTCGATCGGACTAATGCTTGAAACCCAGGACAAATAACCTTATAG	1560
1561	Qy	CTTGTAATTTCTACCAAAATTTGGTGGTTTCAAAATTCGGCTCCGTCGATGTTATACG	1620
1561	Db	CTTGTAATTTCTACCAAAATTTGGTGGTTTCAAAATTCGGCTCCGTCGATGTTATACG	1620
1621	Qy	CCAACTTTGAAACAACTTTTGA AAAAGCTCTTTTCTGGTATTTTAAAGTTTTAGAAATGCAA	1680
1621	Db	CCAACTTTGAAACAACTTTTGA AAAAGCTCTTTTCTGGTATTTTAAAGTTTTAGAAATGCAA	1680
1681	Qy	GGAAACAGTGAATTCGGAGTTCGTTCTTGTTATAATTTAGCTTCTTGCGGGTATCTTTAAATACT	1740
1681	Db	GGAAACAGTGAATTCGGAGTTCGTTCTTGTTATAATTTAGCTTCTTGCGGGTATCTTTAAATACT	1740
1741	Qy	GTAGAAAGAGGAAAGGAAATAATAATTTGGCTTAAATGAGAAATATCACCGGAAATGTGAAAA	1800
1741	Db	GTAGAAAGAGGAAAGGAAATAATAATTTGGCTTAAATGAGAAATATCACCGGAAATGTGAAAA	1800
1801	Qy	ACTGATCGAAAAATACCGCTCGCTTAAAGATACGGAAGGAATGTCCTCTCTAAGCTATA	1860
1801	Db	ACTGATCGAAAAATACCGCTCGCTTAAAGATACGGAAGGAATGTCCTCTCTAAGCTATA	1860
1861	Qy	TAAAGCTGGTGGGAGAAAAATGAAAACCTATATTTAAAAATGACGACAGCCGGTATAAAGG	1920
1861	Db	TAAAGCTGGTGGGAGAAAAATGAAAACCTATATTTAAAAATGACGACAGCCGGTATAAAGG	1920
1921	Qy	GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
1921	Db	GACCACCTATGATGTGGAACGGGAAAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
1981	Qy	TGTTTCAAAGGTCCTGACATTTGAAACCGCATGATGGCTGAGCAATCTGCTCATGAGTGA	2040
1981	Db	TGTTTCAAAGGTCCTGACATTTGAAACCGCATGATGGCTGAGCAATCTGCTCATGAGTGA	2040
2041	Qy	GGCCGATGGCGTCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
2041	Db	GGCCGATGGCGTCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAGATTAT	2100
2101	Qy	CGAGCTGATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGAATGTCCCTA	2160
2101	Db	CGAGCTGATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGAATGTCCCTA	2160
2161	Qy	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATTAACGATCTGGC	2220
2161	Db	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAATTAACGATCTGGC	2220
2221	Qy	CGATGTCGATTGCAAACTCGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
2221	Db	CGATGTCGATTGCAAACTCGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
2281	Qy	TGATTTTTTAAAGACGGAAAAAGCCCGAAGAGGAACCTTGCTTTTTCCACCGGCACCTGGG	2340
2281	Db	TGATTTTTTAAAGACGGAAAAAGCCCGAAGAGGAACCTTGCTTTTTCCACCGGCACCTGGG	2340
2341	Qy	AGACAGCAACATCTTTGTGAAAAGATGCAAGTAAAGTGGCTTTTATGATCTTTGGGAGAAG	2400
2341	Db	AGACAGCAACATCTTTGTGAAAAGATGCAAGTAAAGTGGCTTTTATGATCTTTGGGAGAAG	2400
2401	Qy	CGGCAGGGCGGACAAGTGGTATGACATTTGCTTCTCGCTCGGTCGATCAGGGAGGATAT	2460
2401	Db	CGGCAGGGCGGACAAGTGGTATGACATTTGCTTCTCGCTCGGTCGATCAGGGAGGATAT	2460
2461	Qy	CGGGGAAGAACAGTATGTCGAGCTATTTTTTTGACTTACTGGGATCAAGCTGATTTGGGA	2520
2461	Db	CGGGGAAGAACAGTATGTCGAGCTATTTTTTTGACTTACTGGGATCAAGCTGATTTGGGA	2520
2521	Qy	GAAATAAAAATTTATTTTTTACGTGAATATCTTTTTAGTACTAGATGTGGCGCAACG	2580
2521	Db	GAAATAAAAATTTATTTTTTACGTGAATATCTTTTTAGTACTAGATGTGGCGCAACG	2580

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Db 3661 TGCTGACCCGCTTCCGCGTCTCTGGACCGTGGCAAGAAACGTCCTCCGTTGCCAGGTCTCTGA 3720
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Db 3721 TCACGAGGAAATCGTCTGCTGTTTCTGTCGCCACCACTACACGAAATTCATATGGAGA 3780
QY 3781 AGTACCGCAAGCTGTGCCGACCGCCGACGAGTGTTCGACTATTTTCAGCTCGCACCGGG 3840
Db 3781 AGTACCGCAAGCTGTGCCGACCGCCGACGAGTGTTCGACTATTTTCAGCTCGCACCGGG 3840
QY 3841 AGCGTACCCGCTCAAGCTCGAAACCTTCCGCCCTCATGTGCGATCGATTCACCCGCG 3900
Db 3841 AGCGTACCCGCTCAAGCTCGAAACCTTCCGCCCTCATGTGCGATCGATTCACCCGCG 3900
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Db 3901 TGAAGAGTGGCGGACGAGTGGCGAAGCCTTCCGAGAGTTGCCAGGAGCGGCTGG 3960
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Db 4081 CTGATGGGCTGCTGTATCAGTGGTGTATTTTGTGGGAGCTCGCGTGGGGAGCTGTT 4140
QY 4141 GGCTGGCTGGTGCAGGATATATTTGGTGTAAACAAATTTAGACGCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGCAGGATATATTTGGTGTAAACAAATTTAGACGCTTAGACAACTTAATA 4200
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QY 4261 ATCTAGTAACATATGACACCGCGCGGATAAATTTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATATGACACCGCGCGGATAAATTTATCTAGTTTGGCGCTATATTTTG 4320
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Db 4321 TTTTCTATCGCTATTAATGATATAATTTGGGACTCTAATCAATAAAACCCATCTCAT 4380
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Db 4441 ATGATTAATCATCGACACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAAAATG 4500
QY 4501 TTTTGAACGATCGTTCTGTCGAGCTATGGCCCGA 4533
Db 4501 TTTTGAACGATCGTTCTGTCGAGCTATGGCCCGTA 4533
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RESULT 12

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AAF80291
ID AAF80291 standard; DNA; 7503 BP.
XX AC AAF80291;
XX DT 29-JUN-2001 (first entry)
XX DE Nucleotide sequence of plasmid pMR1203.
XX KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
```

```
XX Synthetic.
OS Key
FH Location/Qualifiers
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FT 655..1263
FT /*tag= b
FT /note= "ori ColE1"
FT 1264..2603
FT /*tag= c
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FT phosphotransferase and kanamycin resistance"
FT 2604..4098
FT /*tag= d
FT /note= "trfA locus from RK2 coding for two proteins P285
FT and P382 enabling an increase in the replication rate"
FT 4106..4271
FT /*tag= e
FT /note= "T-DNA left border"
FT 4272..4559
FT /*tag= f
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FT 4560..5556
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FT /*tag= j
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FT PR2798139-A1.
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX
XX 03-SEP-1999; 99FR-00011112.
XX (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 145-147; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from PRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX Sequence 7503 BP; 1997 A; 1863 C; 1979 G; 1664 T; 0 U; 0 Other;
```





Db 2101 CGAGCTGATGCGAGGTGCATACGGCTCTTTCACTCCATCGACATATCGGATGTCCCTA 2160  
Qy 2161 TACGAATAGCTTACACAGCCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTACACAGCCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC 2220  
Qy 2221 CGATGTGGATTGGCAAACTGGGAAGAGACATCCCATTTAAAGATCCGCGCAGCTGTA 2280  
Db 2221 CGATGTGGATTGGCAAACTGGGAAGAGACATCCCATTTAAAGATCCGCGCAGCTGTA 2280  
Qy 2281 TGAATTTTAAAGACGGAAGCCGGAAGAGGAACTGTCTTTTCCACGCGCACTGGG 2340  
Db 2281 TGAATTTTAAAGACGGAAGCCGGAAGAGGAACTGTCTTTTCCACGCGCACTGGG 2340  
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Qy 2401 CGGAGGGCGGACAAGTGGTATGACATTTGCTCTTCTGCGTCCGFTCGATCAGGAGGATAT 2460  
Db 2401 CGGAGGGCGGACAAGTGGTATGACATTTGCTCTTCTGCGTCCGFTCGATCAGGAGGATAT 2460  
Qy 2461 CGGGGAAGACAGTATGTCAGCTATTTTGTGACTTACTTGGGATCAAGCTGATTTGGGA 2520  
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Qy 2581 ATGCGGCGACAAGAGGAGCGCACCGACTCTTCCGCAATCAAGTGTTTTGGCTCTCAGG 2640  
Db 2581 ATGCGGCGACAAGAGGAGCGCACCGACTCTTCCGCAATCAAGTGTTTTGGCTCTCAGG 2640  
Qy 2641 CCGAGGCCACGGCAAGTATTTGGGCAAGGGTCTGCTGATCAAGTGTTTTGGCTCTCAGG 2700  
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Db |||||||
QY 4381 AATAACGTCATGATACATGTTTAATTAATTAATACATGCTTAACGTAATTAACAGAAATTA 4440
Db |||||||
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Db |||||||
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Db |||||||
QY 4441 ATGATAATATCGCAAGACCGGCAACAGGATTAATCTTAAGAACTTTTATGCGCAATG 4500
Db |||||||
QY 4501 TTTGAACGATCGTTCGTCGAGCTATGCGCCGA 4533
Db |||||||
QY 4501 TTTGAACGATCGTTCGTCGAGCTATGCGCCGA 4533
Db |||||||

RESULT 13
AAF80293
ID AAF80293 standard; DNA; 7503 BP.
XX AC AAF80293;
XX
DT 29-JUN-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pMRT1205.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
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XX
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XX FR2798139-Al.
XX
XX 09-MAR-2001.
XX
XX 03-SEP-1999; 99FR-00011112.
XX

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PR 03-SEP-1999; 99FR-00011112.
XX
PA (MERI-) MERISTEM THERAPEUTICS SA.
XX
XX Gruber V, Comeau D;
XX
XX WPI; 2001-259847/27.
XX
XX New vector free from non-essential elements, useful for transforming
XX cells for protein production and for preparing transgenic plants.
XX
XX Claim 20; Page 153-156; 180pp; French.
XX
XX The specification describes a synthetic vector containing only those
XX elements essential for its functionality and transgenesis of a cell
XX (especially a plant cell). The vector consists of at most one origin of
XX replication (ori), at most one sequence encoding a selection agent and a
XX trfA locus encoding a protein that increases the level of plasmid
XX replication. The vector particularly contains an RK2 ori, especially oriV
XX from PRK2 of Escherichia coli with a broad host range, an antibiotic
XX resistance gene (especially nptIII conferring resistance to kanamycin in
XX bacterial) and a trfA locus from PRK2 encoding the proteins P285 and P382.
XX The vectors are used to prepare transgenic plants and transformed host
XX cells for production of a heterologous proteins, e.g. insulin,
XX interferon, lipase, blood proteins and anti-inflammatory agents. The
XX present sequence represents a plasmid of the invention
XX
XX SQ Sequence 7503 BP; 1998 A; 1863 C; 1979 G; 1663 T; 0 U; 0 Other;
XX
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db |||||||
QY 1 CCGGGCTGTTGCCCTCGCCCTGGGCTGGGCGGCGCTCTATGCCCTGCAGCGCCAG 60
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Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTGCTGCGCTCGGTCGTT	720
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Db	721	CGGCTGCGGAGCGGTATCAGCTCACTCAAAGCGGTAATACGTTTATCCACAGATCA	780
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Qy	841	AAGCCCGCTTGTGCGGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCAAAAAT	900
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Qy	901	CGACGCTCAAGTCAGAGGTGGCAAAACCGACAGGACTATAAAGATACCAAGGCTTTCCC	960
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Qy	961	CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	1020
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Qy	1141	CGCTGCGCTTATCCGGTAACCTATCGTTCAGTCCAAACCGGTGAAGACAGCTATCG	1200
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Qy	1321	AGCGCCATATTTAAAGCTACCAAGACGAAGGATGAAGAGGATGAGGAGGAGATTG	1380
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Qy	1501	GGGCAAGCATATAAACTTCGATGGAATAATGCTTGAACCCAGGACATAAATCTATAG	1560
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Db	1681	GGAACAGTGAATTGGAGTTTCGTTGTATTAATTAAGCTTCTTGGGGTATCTTTAAATACT	1740
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Db	1741	GTAGAAAAGAGGAGGAATAATAAATGCTTAAATCAGAAATACACCGAAATGAAAAA	1800
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Db	1981	TGTTCCAAAGGTCCTGCACCTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA	2040
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Qy	2221	CGATGTGGATTGCGAAAACTGGGAAGAGACACTCCATTTAAAGATCCGCGAGCTGTA	2280
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Qy	2461	CGGGGAAGAACAGTATGTCAGCTATTTTGTGACTTACTGGGGATCAAGCTGATTTGGGA	2520
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Db	2521	GAAATATAAATATATATTTTACTGATGAATTTGTTTTAGTACTAGATGTGCGCAACG	2580
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Db	2581	ATGCGCGGCAACAGCAGGAGCGCACCGACTCTTTCGCGCATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCCAACGCAAGTATTTGGGCAAGGGGTGCTGTTATTCGTCGAGGCAAGATTC	2700
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Db	2701	GGAATACCAAGTACGAAAGGAGCGGACAGCGTCTACGGGACCGACTTCAATTCGCGATA	2760
Qy	2761	AGGTGATTTATCTGGGACACCAAGGCCACAGGCGGGTCAAAATCAGGAATTAAGGCCACATTG	2820

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## RESULT 14

AAF80288  
ID AAF80288 standard; DNA; 8654 BP.

XX AAF80288;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of plasmid pMRT1196.

XX Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;  
XX P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.

XX Synthetic.

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CDS	1264..2603
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CDS	2604..4098

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FT FT and P382 enabling an increase in the replication rate"
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FT XX
FT PF 03-SEP-1999; 99FR-00011112.
FT XX
FT PR 03-SEP-1999; 99FR-00011112.
FT XX
FT PA (MERI-) MERISTEM THERAPEUTICS SA.
FT XX
FT PI Gruber V, Comeau D;
FT XX
FT DR WPI; 2001-259847/27.
FT XX
FT PT New vector free from non-essential elements, useful for transforming
FT FT cells for protein production and for preparing transgenic plants.
FT XX
FT PS Claim 20; Page 132-135; 180pp; French.
FT CC
FT CC The specification describes a synthetic vector containing only those
FT CC elements essential for its functionality and transgenesis of a cell
FT CC (especially a plant cell). The vector consists of at most one origin of
FT CC replication (ori), at most one sequence encoding a selection agent and a
FT CC trfA locus encoding a protein that increases the level of plasmid
FT CC replication. The vector particularly contains an RK2 ori, especially oriV
FT CC from PRK2 of Escherichia coli with a broad host range, an antibiotic
FT CC resistance gene (especially nptII conferring resistance to kanamycin in
FT CC bacteria) and a trfA locus from PRK2 encoding the proteins P285 and P382.
FT CC The vectors are used to prepare transgenic plants and transformed host
FT CC cells for production of a heterologous proteins, e.g. insulin,
FT CC interferon, lipase, blood proteins and anti-inflammatory agents. The
FT CC present sequence represents a plasmid of the invention
FT XX
FT SQ Sequence 8654 BP; 2243 A; 2134 C; 2352 G; 1925 T; 0 U; 0 Other;
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FT Query Match 94.3%; Score 4531.4; DB 4; Length 8654;
FT Best Local Similarity 100.0%; Pred. No. 0;
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FT DB
FT DB 1 CCGGGCTGGTTCCTCGCGCTGGGCTGGCGCGCTATGCGCTGCAAAACGCCCCAG 60
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FT DB 61 AAACGCCGTCGAAGCCGTGTGCAGACACCGCGCGCGCGCTGTGTGATACCTCGGG 120
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QY 781 GGGGTAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAGAAAGGCCAGAAACCGTAAA 840
DB
DB 781 GGGGTAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAGAAAGGCCAGAAACCGTAAA 840
QY 841 AAGGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCGCTGACGAGCATCAAAAAAT 900
DB
DB 841 AAGGCGCGCTTGTGCGGCTTTTCCATAGGCTCCGCCCGCTGACGAGCATCAAAAAAT 900
QY 901 CGACGCTCAAGTCAGAGTGGGCGAAACCCGACAGGACTATAAAGATACAGGGCTTTCCC 960
DB
DB 901 CGACGCTCAAGTCAGAGTGGGCGAAACCCGACAGGACTATAAAGATACAGGGCTTTCCC 960
QY 961 CTTGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCTTCCGCTTACCGATACCTGTCC 1020
DB
DB 961 CTTGGAAGCTCCTCGTGGCTCTCTCTGTTCCGACCTTCCGCTTACCGATACCTGTCC 1020
QY 1021 GCCTTTCTCCCTTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
DB
DB 1021 GCCTTTCTCCCTTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
QY 1081 TCGGTGTAGTGTGCTTCCAGTGTGGCTGTGTGCAAGAACCCCGCTTTCAGCCCGAC 1140
DB
DB 1081 TCGGTGTAGTGTGCTTCCAGTGTGGCTGTGTGCAAGAACCCCGCTTTCAGCCCGAC 1140
QY 1141 CGCTGCGCTTATCCGTTAACTATCGTCTTGAAGTCCAAACCCCGTAAAGACGACTTATCG 1200
DB
DB 1141 CGCTGCGCTTATCCGTTAACTATCGTCTTGAAGTCCAAACCCCGTAAAGACGACTTATCG 1200
QY 1201 CCACTGGCAGCAGCCTTCTACCATTAATCCGCGATAAACCCAGCAACCACTTTGAGGTGAT 1260
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1201	Db	 C C A C T G C C A G C A G C T T C T A C C A T A A T C C C G G A T A A A C C C A G C G A A C C A T T T C A G G T G A T	1260
1261	Qy	 A G G T A G A T T A T A C C G A G G T A T G A A A C G A G A A T T G G A C C T T T A C A G A A T T A C T C T A T A G A	1320
1261	Db	 A G G T A G A T T A T A C C G A G G T A T G A A A C G A G A A T T G G A C C T T T A C A G A A T T A C T C T A T A G A	1320
1321	Qy	 A G G C C A T A T T T A A A A G C T A C C A A G A C G A A G G A T G A A G A G A T T A A G A G A T T A G A G A G C A G A T T G	1380
1321	Db	 A G G C C A T A T T T A A A A G C T A C C A A G A C G A A G G A T G A A G A G A T T A A G A G A T T A G A G A G C A G A T T G	1380
1381	Qy	 C C T T G A A T A T T T G A C A A T A C T G A T A A G A T A A T A C A T C T T T T T A T A T A G A A G A T A T C G C C G	1440
1381	Db	 C C T T G A A T A T T T G A C A A T A C T G A T A A G A T A A T A C A T C T T T T A T A T A G A A G A T A T C G C C G	1440
1441	Qy	 T A T G T A A G A T T T C A G G G G C A A G G C A T A G G C A G C G C T T A T C A A T A T A T C T A T A G A A T	1500
1441	Db	 T A T G T A A G A T T T C A G G G G C A A G G C A T A G G C A G C G C T T A T C A A T A T A T C T A T A G A A T	1500
1501	Qy	 G G G C A A A G C A T A A A A C T T C A T G A G A C T A A T G C T T G A A A C C C A G G A C A A T A A C C T T A T A G	1560
1501	Db	 G G G C A A A G C A T A A A A C T T C A T G A T G A A C T A A T G C T T G A A A C C C A G G A C A A T A A C C T T A T A G	1560
1561	Qy	 C T T G T A A A T T C T A C C A A A A T T G T G G T T C A A A A T C G G C T C C G T C G A T A C T A T G T T A T A C G	1620
1561	Db	 C T T G T A A A T T C T A C C A A A A T T G T G G T T C A A A A T C G G C T C C G T C G A T A C T A T G T T A T A C G	1620
1621	Qy	 C C A A C T T T G A A A C A A C T T T G A A A A A C G T T T C T G T A T T T A A G G T T T A G A A T G C A A	1680
1621	Db	 C C A A C T T T G A A A C A A C T T T G A A A A A C G T T T C T G T A T T T A A G G T T T A G A A T G C A A	1680
1681	Qy	 G G A C A G T G A A T T C G A G T T C G T C T T G T T A A A T T A G C T T C T G G G G T A C T T T A A A T A C T	1740
1681	Db	 G G A C A G T G A A T T C G A G T T C G T C T T G T T A A A T T A G C T T C T G G G G T A C T T T A A A T A C T	1740
1741	Qy	 G T A G A A A G A G G A A G A A A T A A A T T G C T T A A A T G A G A A T A C A C C G A A T T G A A A A	1800
1741	Db	 G T A G A A A G A G G A A G A A A T A A A T T G C T T A A A T G A G A A T A C A C C G A A T T G A A A A	1800
1801	Qy	 A C T G A T C G A A A A T A C C G C T G C G T A A A A G A T A C G A A G A A T G T C T C T C T A A G G T A T A	1860
1801	Db	 A C T G A T C G A A A A T A C C G C T G C G T A A A A G A T A C G A A G A A T G T C T C T C T A A G G T A T A	1860
1861	Qy	 T A A G C T G T G G G A A A A T G A A A C C T A T A T T T A A A A A T G A C G A C A G C C G G T A T A A A G G	1920
1861	Db	 T A A G C T G T G G G A A A A T G A A A C C T A T A T T T A A A A A T G A C G A C A G C C G G T A T A A A G G	1920
1921	Qy	 G A C C A C C T A T G A T T G G A A C G G G A A A A G G A C A T A T G C T A T G G T C T G A A G A A A G C T G C C	1980
1921	Db	 G A C C A C C T A T G A T T G G A A C G G G A A A A G G A C A T A T G C T A T G G T C T G A A G A A A G C T G C C	1980
1981	Qy	 T G T T C C A A A A G T C T G C A C T T T G A A C C G C A T G A T G C T G A G A G A A T C T G C T A T G A G T A	2040
1981	Db	 T G T T C C A A A A G T C T G C A C T T T G A A C C G C A T G A T G C T G A G A G A A T C T G C T A T G A G T A	2040
2041	Qy	 G G C C G A T G G C G T C T T T C T C G G A A G A G A T G A A G A T G A A C A A A G C C C T G A A A A G A T T A T	2100
2041	Db	 G G C C G A T G G C G T C T T T T C T C G G A A G A G A T G A A G A T G A A C A A A G C C C T G A A A A G A T T A T	2100
2101	Qy	 C G A G C T G T A T G C G A G T G C A T C A G G C T C T T T C A C T C C A T C G A C A T A T C G G A T T G T C C C T A	2160
2101	Db	 C G A G C T G T A T G C G A G T G C A T C A G G C T C T T T C A C T C C A T C G A C A T A T C G G A T T G T C C C T A	2160
2161	Qy	 T A C G A A T A G C T T A G A C A G C C G C T T A G C G A A T T G G A T T A C T T A C T G A A T A A C G A T C T G G C	2220
2161	Db	 T A C G A A T A G C T T A G A C A G C C G C T T A G C G A A T T G G A T T A C T T A C T G A A T A A C G A T C T G G C	2220
2221	Qy	 C G A T G T G A T T G C G A A A C T C G G A A G A G A C A C T C C A T T T A A A C A T C C G C G A G C T G T A	2280
2221	Db	 C G A T G T G A T T G C G A A A C T C G G A A G A A G A C A C T C C A T T T A A A G A T C C G C G A G C T G T A	2280
2281	Qy	 T G A T T T T T T A A A A G A C G G A A A A G C C C A A G A G A A C T T G T C T T T T T C C A C C G C G A C T G G G	2340

2281	TGATTTTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTTCCCAACGGCGACCTGGG	2340
2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTGATCTTTGGAGAAG	2400
2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTGATCTTTGGAGAAG	2400
2401	CGGCAAGGCGGACAAGTGGTATGACATTTGCTTCTTGGTCCGGTCCGATCAGGAGGAGTAT	2460
2401	CGGCAAGGCGGACAAGTGGTATGACATTTGCTTCTTGGTCCGGTCCGATCAGGAGGAGTAT	2460
2461	CGGGGAAGAACAGTATCTGCAGCTATTTTTTGACTTACTTGGGGATCAAGCCTGATTCGGGA	2520
2461	CGGGGAAGAACAGTATCTGCAGCTATTTTTTGACTTACTTGGGGATCAAGCCTGATTCGGGA	2520
2521	GAATAATAATATTATATTTTACTTGGATGAATTTGTTTGTAGTACCTAGATGTGGCGCAACG	2580
2521	GAATAATAATATTATTTTACTTGGATGAATTTGTTTGTAGTACCTAGATGTGGCGCAACG	2580
2581	ATGCCGGCGACAAGCAGGAGCGACCGACTTCTTCGGATCAAGTGTGTTTGGCTCTCAGG	2640
2581	ATGCCGGCGACAAGCAGGAGCGACCGACTTCTTCGGATCAAGTGTGTTTGGCTCTCAGG	2640
2641	CCGAGGCCACCGCAAGTATTTGGGCAAGGGGTCCCTCGTATTTCTGTGCAGGCGCAAGATTC	2700
2641	CCGAGGCCACCGCAAGTATTTGGGCAAGGGGTCCCTCGTATTTCTGTGCAGGCGCAAGATTC	2700
2701	GGATACCAAGTACGAGAAGACGGCCAGACGGTCTTACGGACCGACTTCATTCCCGGATA	2760
2701	GGATACCAAGTACGAGAAGACGGCCAGACGGTCTTACGGACCGACTTCATTCCCGGATA	2760
2761	AGGTGGATTATCTGGACACCAAGGCAACAGCGGGGTCAAAATCAGGAATAAGGGCACATTG	2820
2761	AGGTGGATTATCTGGACACCAAGGCAACAGCGGGGTCAAAATCAGGAATAAGGGCACATTG	2820
2821	CCCCGGCTGAGTGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTCACCGGA	2880
2821	CCCCGGCTGAGTGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTCACCGGA	2880
2881	AGGCATACAGGCAGAACTGATCGACCGCGGGTTTTCCGCGAGGATCCGAAACCATCG	2940
2881	AGGCATACAGGCAGAACTGATCGACCGCGGGTTTTCCGCGAGGATCCGAAACCATCG	2940
2941	CAAGCGCACCGTCAATGCGTCCGCGCGAAACCTTCCAGTCCGTCGGCTCGATGCTCC	3000
2941	CAAGCGCACCGTCAATGCGTCCGCGCGAAACCTTCCAGTCCGTCGGCTCGATGCTCC	3000
3001	AGCAAGCTACCGCCCAAGTACGAGCGGACAGCTGCACTGCTCCCTCCCTCCCTGCCCC	3060
3001	AGCAAGCTACCGCCCAAGTACGAGCGGACAGCTGCACTGCTCCCTCCCTCCCTGCCCC	3060
3061	CGGCATTCGCGCGCGTGGAGCGTTTCGCGTTCGTCTCGAAACGAGGCGGCGAGTTTGGCGA	3120
3061	CGGCATTCGCGCGCGTGGAGCGTTTCGCGTTCGTCTCGAAACGAGGCGGCGAGTTTGGCGA	3120
3121	AGTCGATGACCATCGACACGCGAGGAACCTATGACGACCAAGAGCGAAACACCGCGCGG	3180
3121	AGTCGATGACCATCGACACGCGAGGAACCTATGACGACCAAGAGCGAAACACCGCGCGG	3180
3181	AGGACCTGCGCAAAACAGGTACGAGGCGCAAGCAGCGCGCGTTCGTGAACACACGAAAGC	3240
3181	AGGACCTGCGCAAAACAGGTACGAGGCGCAAGCAGCGCGCGTTCGTGAACACACGAAAGC	3240
3241	AGCAGATCAAGGAATGACGCTTTCCTTGTTCATATTCGCGCGTGGCGGACACGATGC	3300
3241	AGCAGATCAAGGAATGACGCTTTCCTTGTTCATATTCGCGCGTGGCGGACACGATGC	3300
3301	GAGCGATGCGCAAAACGACCGCGCGTCTCGCTGTTTCAACGCGCGAACAGAAATATCC	3360
3301	GAGCGATGCGCAAAACGACCGCGCGTCTCGCTGTTTCAACGCGCGAACAGAAATATCC	3360
3361	CGCGAGGCGCTGCAAAACAAAGTCAATTTTCCACGTCAACAGGACGTGAGATCACT	3420
3361	CGCGAGGCGCTGCAAAACAAAGTCAATTTTCCACGTCAACAGGACGTGAGATCACT	3420



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QY 3421 ACACCGCGTCGAGCTGCGCGCCGACGATACGAACCTGGTGTGCGCAGCAGTGTGAGT 3480
Db 3421 ACACCGCGTCGAGCTGCGCGCCGACGATACGAACCTGGTGTGCGCAGCAGTGTGAGT 3480
QY 3481 ACCGAGCGACCCCTATCGCGAGCGCGATCACTTCAGTTCCTACGAGCTTTGCCAGG 3540
Db 3481 ACCGAGCGACCCCTATCGCGAGCGCGATCACTTCAGTTCCTACGAGCTTTGCCAGG 3540
QY 3541 ACCTGGGCTCGTCGATCAATGGCGGCTATTACAGAAAGCCGAGGAATGCTGTCGCGCC 3600
Db 3541 ACCTGGGCTCGTCGATCAATGGCGGCTATTACAGAAAGCCGAGGAATGCTGTCGCGCC 3600
QY 3601 TACAGGCGACGGCGATGGGCTTACGTCGACCGCGTGGGACACCTGGGAATCGGTGTGCG 3660
Db 3601 TACAGGCGACGGCGATGGGCTTACGTCGACCGCGTGGGACACCTGGGAATCGGTGTGCG 3660
QY 3661 TGGTCACCGCTTCCGGCTCTCGACCGTGGCGGAAGAAAGTCCGTTGCCAGGCTCTGA 3720
Db 3661 TGGTCACCGCTTCCGGCTCTCGACCGTGGCGGAAGAAAGTCCGTTGCCAGGCTCTGA 3720
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Db 3841 AGCGGTACCGCTCAAGCTGGAAACCTTCGCGCTCATGTGCGGATCGGAATCCACCGCG 3900
QY 3901 TGAAGAAGTGGCGGAGCAGCTCGCGAAGCCTGCGAAGTTCGAGGCGAGCGGCTGG 3960
Db 3901 TGAAGAAGTGGCGGAGCAGCTCGCGAAGCCTGCGAAGTTCGAGGCGAGCGGCTGG 3960
QY 3961 TGAACAACGCTGGGTCAATGATGACCTGGTGATTTGCAACGCTAGGGCTTTGTGGGT 4020
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Db 4021 CAGTTCGGCTGGGGTTACGAGCAGCGCTTTACTGGCATTTCTAGTTGACGCTTT 4080
QY 4081 CTGATCGGCTGCCTGTATCGAGTGGTATTTTGTGCGGAGCTCGCGTGGGAGCTGTT 4140
Db 4081 CTGATCGGCTGCCTGTATCGAGTGGTATTTTGTGCGGAGCTCGCGTGGGAGCTGTT 4140
QY 4141 GGCTGCTGGTGGCAGGATATATTGTGTAAACAAATTTGACCTTAGACAACTTAATA 4200
Db 4141 GGCTGCTGGTGGCAGGATATATTGTGTAAACAAATTTGACCTTAGACAACTTAATA 4200
QY 4201 ACATATTGGGAGCTTTTAAATGATCTGGGCTATCCCGGGGATATCCATAGCCCG 4260
Db 4201 ACATATTGGGAGCTTTTAAATGATCTGGGCTATCCCGGGGATATCCATAGCCCG 4260
QY 4261 ATCTAGTAACATAATCACACCGCGGATATTTATCTAGTTTGGCGCTATATTTG 4320
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QY 4321 TTTTCTATCGGCTATTAATGATATGTCGGGACTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGGCTATTAATGATATGTCGGGACTCTAATCATATAAAACCCATCTCAT 4380
QY 4381 AATAAGCTCATGATTAATGATTAATTAATGATTAATGATTAATGATTAATGATTAAT 4440
Db 4381 AATAAGCTCATGATTAATGATTAATTAATGATTAATGATTAATGATTAATGATTAAT 4440
QY 4441 ATGATTAATCATCGCAGACCGGCAACAGGATTCATCTTAAGAACTTTATGCGCAATG 4500
Db 4441 ATGATTAATCATCGCAGACCGGCAACAGGATTCATCTTAAGAACTTTATGCGCAATG 4500
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QY 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533

RESULT 15
AAF80296
ID AAF80296 standard; DNA; 8987 BP.
XX
AC AAF80296;
XX
DT 29-JUN-2001 (first entry)
XX
Nucleotide sequence of plasmid pMT1212.
DE
XX
Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
P382 protein; antibiotic resistance gene; nptIII; transgenic plant; ss.
XX
Synthetic.
XX
Key Location/Qualifiers
FT rep_origin 1..654
FT /tag= a
FT /note= "ori RK2"
FT rep_origin 655..1263
FT /tag= b
FT /note= "ori ColE1"
FT CDS 1264..2603
FT /tag= c
FT /note= "NPT III gene coding for neomycin
phosphotransferase and kanamycin resistance"
FT CDS 2604..4098
FT /tag= d
FT /note= "TrfA locus from RK2 coding for two proteins P285
and P382 enabling an increase in the replication rate"
FT terminator 4272..4559
FT /tag= e
FT /note= "nopaline synthetase terminator"
FT CDS 4575..5150
FT /tag= f
FT /note= "Bar gene coding for phosphinotricin
acetyltransferase and glufosinate resistance"
FT promoter 5151..5368
FT /tag= g
FT /note= "nopaline synthetase promoter"
FT promoter 5369..6111
FT /tag= h
FT /note= "enhanced promoter from 35S ribosome"
FT CDS 6159..8050
FT /tag= i
FT /note= "GUS gene coding for beta glucuronidase"
FT polyA_signal 8051..8780
FT /tag= j
FT /note= "polyA from 35S ribosome"
FT misc_feature 8807..8980
FT /tag= k
FT /note= "T-DNA right border"
XX
FR2798139-A1.
XX
09-MAR-2001.
XX
03-SEP-1999; 99FR-00011112.
XX
03-SEP-1999; 99FR-00011112.
XX
(MERI-) MERISTEM THERAPEUTICS SA.
XX
Gruber V, Comeau D;
XX
WPI; 2001-259847/27.
XX
New vector free from non-essential elements, useful for transforming
PT
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cells for protein production and for preparing transgenic plants.

Claim 20; Page 168-171; 180pp; French.

The specification describes a synthetic vector containing only those elements essential for its functionality and transgenesis of a cell (especially a plant cell). The vector consists of at most one origin of replication (ori), at most one sequence encoding a selection agent and a trfA locus encoding a protein that increases the level of plasmid replication. The vector particularly contains an RK2 ori, especially oriV from *PK2* of *Escherichia coli* with a broad host range, an antibiotic resistance gene (especially *npIII* conferring resistance to kanamycin in bacteria) and a trfA locus from *PK2* encoding the proteins P285 and P382. The vectors are used to prepare transgenic plants and transformed host cells for production of a heterologous proteins, e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory agents. The present sequence represents a plasmid of the invention

Sequence 8987 BP; 2342 A; 2205 C; 2438 G; 2002 T; 0 U; 0 Other;

94.3%; Score 4531.4; DB 4; Length 8987; every Match

Best Local Similarity 100.0%; Pred. No. 0;

Sequence	Conservative	Mismatches	Indels	Gaps
Sequence 1	4532	0	1	0
Sequence 2	4532	0	1	0

1	CGGGCTGGTTCGCTCCGCGCTGGGTGGGGCGCTCTATTGGCCCTCGCAACGGCCGAG	60
1	CGGGCTGGTTCGCTCCGCGCTGGGTGGGGCGCTCTATTGGCCCTCGCAACGGCCGAG	60
61	AAACCGCGTCGAAGCGGTGTGCGAGACACCGCGGCGCGCGTGTGTGATACCTTCGCGG	120
61	AAACCGCGTCGAAGCGGTGTGCGAGACACCGCGGCGCGCGTGTGTGATACCTTCGCGG	120
121	AAAACTTGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTTGAGGGGCGACTCAC	180
121	AAAACTTGCCCTCACTGACAGATGAGGGCGGAGCGTTGACACTTTGAGGGGCGACTCAC	180
181	CGGGCGCGCGTGTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGAGCTGGAGCTGGC	240
181	CGGGCGCGCGTGTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGAGCTGGAGCTGGC	240
241	CAGCTTCGCAAAATCGCGCAAAACGCTGATTTTACCGAGTTTCCACAGATGATGTGGA	300
241	CAGCTTCGCAAAATCGCGCAAAACGCTGATTTTACCGAGTTTCCACAGATGATGTGGA	300
301	CAAGCTCGGGGATAGTGCCTCGGCTATTGACACTTGAGGGGCGCGACTACTGACAGAT	360
301	CAAGCTCGGGGATAGTGCCTCGGCTATTGACACTTGAGGGGCGCGACTACTGACAGAT	360
361	GAGGGCGCGATCCTTTGACACTTGAGGGCGAGAGTCTGACAGATGAGGGGCGCACTTAT	420
361	GAGGGCGCGATCCTTTGACACTTGAGGGCGAGAGTCTGACAGATGAGGGGCGCACTTAT	420
421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCAATTTGCAAGGGTTTCCGCCCGT	480
421	TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCAATTTGCAAGGGTTTCCGCCCGT	480
481	TTTTGGGCGACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTATTAACCTTG	540
481	TTTTGGGCGACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTATTAACCTTG	540
541	TTTTTAACAGGGCTCGGCCCTGTGCGCGTGACCGCGCACCGCGAAGGGGGTGCCTCCC	600
541	TTTTTAACAGGGCTCGGCCCTGTGCGCGTGACCGCGCACCGCGAAGGGGGTGCCTCCC	600
601	CTTCTCGAACCCCTCCCGGAAAGGATGCGGGTGTGAATAACCGCACAGATGCGTAAGGAGA	660
601	CTTCTCGAACCCCTCCCGGAAAGGATGCGGGTGTGAATAACCGCACAGATGCGTAAGGAGA	660
661	AAATACCGGATCAGGGCGCTTCTCCGCTTCTCGCTCACCTGCTCGCTCGCTCGGTGCTT	720
661	AAATACCGGATCAGGGCGCTTCTCCGCTTCTCGCTCACCTGCTCGCTCGCTCGGTGCTT	720
721	CGGCTCGGGCGAGCGGTATCAGCTCACTCAAAGGGCGGTAATACGGTTATTCCACAGAATCA	780

Db 1801 ACTGATCGAAAAATAACCGCTCGTAAAGATACGGAAGGAATGTCTCTCTGAAGTATA 1860  
Qy 1861 TAAGCTGGTGGAGAAAATGAAGAACTATATTTAAAAATGACGACAGCGCGGTATAAAGG 1920  
Db 1861 TAAGCTGGTGGAGAAAATGAAGAACTATATTTAAAAATGACGACAGCGCGGTATAAAGG 1920  
Qy 1921 GACCACTATGATGTGAAACGGGAAAAAGGACATGATGCTATGCTGGAAGAAAGCTGCC 1980  
Db 1921 GACCACTATGATGTGAAACGGGAAAAAGGACATGCTATGCTGGAAGAAAGCTGCC 1980  
Qy 1981 TGTTCCAAAGGTCTGACATTTGAAACGGCATGATGGCTGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCCAAAGGTCTGACATTTGAAACGGCATGATGGCTGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGGCGATGGCGTCTCTTTGCTCGGAAGAGTAGTAAGATGAACAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGGCGATGGCGTCTCTTTGCTCGGAAGAGTAGTAAGATGAACAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA 2160  
Db 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTA 2160  
Qy 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATAACGATCTGGC 2220  
Db 2161 TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATAACGATCTGGC 2220  
Qy 2221 CGATGTGGATTGCGAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGCGAGCTGTA 2280  
Db 2221 CGATGTGGATTGCGAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGCGAGCTGTA 2280  
Qy 2281 TGAATTTTTAAAGACGGAAAGCCCGAAGAGGAACCTTTGCTCTTTCCACGCGACCTGGG 2340  
Db 2281 TGAATTTTTAAAGACGGAAAGCCCGAAGAGGAACCTTTGCTCTTTCCACGCGACCTGGG 2340  
Qy 2341 AGACAGCAACATCTTTGTGAAAAGATGCAAAAGTAAGTGGCTTTATTTGATCTTGGGGAAG 2400  
Db 2341 AGACAGCAACATCTTTGTGAAAAGATGCAAAAGTAAGTGGCTTTATTTGATCTTGGGGAAG 2400  
Qy 2401 CGGAGGCGGACAAAGTGTATGACATTTGCTCTGCTCGCTCCGCTCGATCAGGAGGATAT 2460  
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Qy 2461 CGGGGAAGAACAGTATGTCAGCTATTTTTTGACTTACTCGGGATCAAGCTGATTTGGGA 2520  
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Db	4261		4320
Qy	4321	TTTTCTATCGGTAATTAATGTATAATTCGGGACTCTAATCATATAAAACCCATCTCATA	4380
Db	4321		4380
Qy	4381	AATAACGTCATGCATTACATGTTAATTATACATGCTTAACGTAATTCACAGAAATTAT	4440
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Qy	4441	ATGATAATCATCGCAAGACCGGCAACAGGATTCAATCTTAAGAACTTTATTGCCAAATG	4500
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Qy	4501	TTTGAACGATCGTTTCGTGAGCTATGGCCCGA	4533
Db	4501		4533

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC  
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2522.2	52.5	13737	4	US-09-538-414-10
3	2522.2	52.5	13737	4	US-10-074-279-10
C 4	1393	29.0	10323	4	US-09-280-428A-11
C 5	1393	29.0	14113	3	US-09-223-134-1
C 6	1393	29.0	14113	3	US-08-992-801-1
C 7	1393	29.0	14113	3	US-09-223-535-1
8	1025.2	21.3	4161	4	US-09-185-244-8
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19	592	12.3	3122	3	US-09-042-353-152
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C 45	592	12.3	5013	4	US-09-183-188B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-948-138-4/c  
; Sequence 4, Application US/09948138  
; Patent No. 6534695

; GENERAL INFORMATION:  
; APPLICANT: AGRINOMICS, LLC

; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A DWARF AND LATE FLOWERING  
; FILE OF INVENTION: PHENOTYPE (DLF2) IN ARABIDOPSIS  
; FILE REFERENCE: AG01006C

; CURRENT APPLICATION NUMBER: US/09/948,138  
; CURRENT FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: US60/230340  
; PRIOR FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4  
; LENGTH: 12241

; TYPE: DNA  
; ORGANISM: vector, multiple sequences

US-09-948-138-4

Query Match 52.8%; Score 2536.2; DB 4; Length 12241;  
Best Local Similarity 76.6%; Pred. No. 0;  
Matches 3505; Conservative 0; Mismatches 558; Indels 514; Gaps 12;

QY	1	CCGGGCTGGTTGCCCTCGCGCTGGCGCTGGCGCCCTCTATGGCCCTGCAACGCGCCAG	60
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QY	181	CCGGCGCGGCTTGACAGATGAGGGCGGCGAGCTCGATTTCGGCGCGGCGAGCTGGAGCTGGC	240
DB	12061	CCGGCGCGGCTTGACAGATGAGGGCGGCGAGCTCGATTTCGGCGCGGCGAGCTGGAGCTGGC	12002
QY	241	CAGCTTCGCAAAATCGCGGAAAACGCGCTGATTTACCGAGTTTCCACAGATGATGTGA	300
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QY	301	CAAGCCTGGGATTAAGTGCCTCGCGTATTTGACACTTGAGGGCGGCGACTTACTGACAGAT	360
DB	11941	CAAGCCTGGGATTAAGTGCCTCGCGTATTTGACACTTGAGGGCGGCGACTTACTGACAGAT	11882
QY	361	GAGGGCGCGATCCTTTGACACTTGAGGGCGGAGAGTCTGACAGATGAGGGCGGCGACCTAT	420







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; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-09-538-414-10

Query Match      52.5%; Score 2522.2; DB 4; Length 13737;
Best Local Similarity 76.5%; Pred. No. 0;
Matches 3505; Conservative 0; Mismatches 558; Indels 518; Gaps 13;

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Qy      61  AAGCCGCTGAAGCCGTGTGCGAGACCG- - - - -CGGCGCGCGCGGTGTGTGGATACCTC 116
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Qy      117 GCGGAAACCTGGCCCTCACTGACAGATGAGGCGGCGGCTTGACACTTGAGGGGCGGAC 176
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Qy      477 CCGTTTTTCGCGCACCGCTAACCTGTCTTTTAACTCTTTTAAACCAATATTTATAAC 536
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Qy      619 - - - - -
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Qy      770 CC- - - - -
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Qy      772 - - - - -
Db      5271 GCGGCAATTTTACCTTGGGCATTTCTTGGCAATTTACTCTATGAAGCGCATATTTAAAGGCTAC 5330

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Db      5331 CCGGGGTGCGATAAACCCAGCAACCAATTTGAGGTGATAGGTAAATATACCGAGTAT 5390

Qy      809 CAAAAGG- - - - -
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Qy      816 - - - - -
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Db      5511 GATAAGATAATATATCTTTTATATAGAGATATCGCGTATGTAAAGATTTACGGGGGCA 5570

Qy      862 TTCATAGGCTCCGC- - - - -
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Qy      877 - - - - -CCCCCTGACGAGCATCAAAATATCGAGCTCAAGTCAGAGTG 920
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Qy      935 - - - - -GACTATAAAGATACACAGCGGTTTCCCTTGGAAAGCTCCCTCGTCCGC 981
Db      5751 ATGAGCTCCACCGATTTTGAGAAACGACAGCACTTCCGTCGCCAGCGTCCAGGTGCTG 5810

Qy      982 TCTCTGTTCCGACCCCTGCGGCT-TACCGGATACGTGTCGCGCTTTCTCCCTTCGGAAG 1040
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Qy      1041 CGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGTTGAGGTGCTTCGCTC 1100
Db      5871 CTTTCCCTTCAGGGGGAATTCATACAGCGGCGAGCATCCGTCATCATATCACCACGTC 5930

Qy      1101 CAAGCTGGGCTGTGTGCACGAA- - - - -CCCCCGGTTTCAGGCCCGACCGCTCGGCTTATCC 1155
Db      5931 AAAGGTGACAGAGGCTCATAGACGCCCGCCAGCTGCGCCATAGTGTGCTTCCACGAATAC 5990

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Qy      1336 AAGTACCAAGACGAGAGGATGAAGAGGATGAGGAGGAGATTGCCCTTGAATATATGA 1395
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Qy	1528	TAATGCTTGAACCCAGGACA---ATAACCTTATAGCTTGTAAATCTCAAAATTTGTG	1584
Db	6409	CACCTCAAAACACCATACATACATAAATCAGTAAGTTGGCAGCATCACCCATAAATTTGTG	6468
Qy	1585	GTTTCAAAATCCGCTCCGTCGATACTATGTATACGCCAATTTTGAATAACACTTTGAAA	1644
Db	6469	GTTTCAAAATCCGCTCCGTCGATACTATGTATACGCCAATTTTGAATAACACTTTGAAA	6528
Qy	1645	AAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAAGGACACAGTGAATTTGGAGTTCTGCT	1704
Db	6529	AAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAAGGACACAGTGAATTTGGAGTTCTGCT	6588
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Db	6589	TGTTATAATTAGCTTTCTGGGTATCTTTAAATACTGTAGAAAGAGGAAAGAAATAATA	6648
Qy	1765	AATGGCTTAAATGAGATATCACCGNAATTTGAAAACCTGATCGAAAATACCGTGCCT	1824
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Qy	1945	AAAGGACATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGTCTCTGCACCTTGA	2004
Db	6829	AAAGGACATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGTCTCTGCACCTTGA	6888
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Db	6889	ACGCGATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCGGATGGCGTCTTTGCTCGGA	6948
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Db	6949	AGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGCAATCAG	7008
Qy	2125	GCTCTTTCACTCCATCGACATATCGGATTTGCTTCCCTATACGAATAGCTTAGACAGCCGCTT	2184
Db	7009	GCTCTTTCACTCCATCGACATATCGGATTTGCTTCCCTATACGAATAGCTTAGACAGCCGCTT	7068
Qy	2185	AGCGGAATTCGATTACTTACTGATTAACAGATCTGGCCGATGTGGATTTCGAAAACCTGGGA	2244
Db	7069	AGCGGAATTCGATTACTTACTGATTAACAGATCTGGCCGATGTGGATTTCGAAAACCTGGGA	7128
Qy	2245	AGAAGACACTCCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGGCC	2304
Db	7129	AGAAGACACTCCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGGCC	7188
Qy	2305	CGAAGAGAACTTGTCTTTTCCACCGCGACTGGGAGACAGCAACATCTTTGTGAAGA	2364
Db	7189	CGAAGAGAACTTGTCTTTTCCACCGCGACTGGGAGACAGCAACATCTTTGTGAAGA	7248
Qy	2365	TGCAAAAGTAAGTGGCTTTTATTCATCTTGGAGAGAGCGGACGAGGAGGATGA	2424
Db	7249	TGGCAAGTAAGTGGCTTTTATTCATCTTGGAGAGAGCGGACGAGGAGGATGA	7308
Qy	2425	CATTGGCTTCTCGGTCGATCAGGGAGGATATCGGGGAAGAACAGTATGTCGAGCT	2484

Db	7309	CATTGGCTTCTGGCTCCGCTCGATCAGGGAGGATATCGGGAAAGAACAGTATGTCGAGCT	7368
Qy	2485	ATTTTTTGACTTACTCGGGATCAAGCTGATTCGGAGAAAATAAAATATTATATTTTACT	2544
Db	7369	ATTTTTTGACTTACTCGGGATCAAGCTGATTCGGAGAAAATAAAATATTATATTTTACT	7428
Qy	2545	GGATGAATTTGTTTTAGTACCTAGATGTGGCGCAACGATGCGCGACAAAGCAGAGAGCGCA	2604
Db	7429	GGATGAATTTGTTTTAGTACCTAGATGTGGCGCAACGATGCGCGACAAAGCAGAGAGCGCA	7488
Qy	2605	CGACTTCTTCCGATCAAGTGTTTTGGCTCTCAGCGCGAGGCCCAAGGCAAGTATTGG	2664
Db	7489	CCGACTTCTTCCGATCAAGTGTTTTGGCTCTCAGCGCGAGGCCCAAGGCAAGTATTGG	7548
Qy	2665	GCAGGGGTGCGTGTATTTCGTCAGCGGCAAGATTCGGAATACCAAGTACGAGAAGACG	2724
Db	7549	GCAAGGGGTGCGTGTATTTCGTCAGCGGCAAGATTCGGAATACCAAGTACGAGAAGACG	7608
Qy	2725	GCAGAGCGGTCTACGGGACCGACTTTCATTTGCCGATTAAGGTGGATTTATCTCGACACCAAGG	2784
Db	7609	GCCAGACGGTCTACGGGACCGACTTTCATTTGCCGATTAAGGTGGATTTATCTCGACACCAAGG	7668
Qy	2785	CACAGCGGGTCAAAATCAGGAATAAGGGCACATTTGCCCGCGTGTAGTCTGGGCAATCC	2844
Db	7669	CACCAGCGGGTCAAAATCAGGAATAAGGGCACATTTGCCCGCGTGTAGTCTGGGCAATCC	7728
Qy	2845	CGCAAGGAGGTCAATGAATTCGGACCGTTCGACCGAAGGATACAGGCAAGAACTGATCG	2904
Db	7729	CGCAAGGAGGTCAATGAATTCGGACCGTTCGACCGAAGGATACAGGCAAGAACTGATCG	7788
Qy	2905	ACGCGGGTTTTCCGCGCAGGATGCGGAAACCAATCGCAAGCCGACCGTCATCGTGC	2964
Db	7789	ACGCGGGTTTTCCGCGCAGGATGCGGAAACCAATCGCAAGCCGACCGTCATCGTGC	7848
Qy	2965	CCCGGAAACCTTTCAGTTCGCTCGGTTCGATGTCCAGCAAGCTACGGCCAAAGATCAGC	3024
Db	7849	CCCGGAAACCTTTCAGTTCGCTCGGTTCGATGTCCAGCAAGCTACGGCCAAAGATCAGC	7908
Qy	3025	GGCAGACGTCGAACCTTGGCTCCCTGCTGCGCGGATCGGCGGATCGGCGGCTGGAGCGTT	3084
Db	7909	GCACAGCGTGCACTTGGCTCCCTGCTGCGCGGATCGGCGGATCGGCGGCTGGAGCGTT	7968
Qy	3085	CGCGTCTCTCGAAACAGGAGCGCGGAAAGTTTGGCGAAGTCCGATGACCATCGACACGCGAG	3144
Db	7969	CGCGTCTCTCGAAACAGGAGCGCGGAAAGTTTGGCGAAGTCCGATGACCATCGACACGCGAG	8028
Qy	3145	GAACTATGACGACCAAGAGCGAAAAACCGCGCGGAGGACCTGGCAAAAACAGGTCAGCG	3204
Db	8029	GAACTATGACGACCAAGAGCGAAAAACCGCGCGGAGGACCTGGCAAAAACAGGTCAGCG	8088
Qy	3205	AGGCCAAGCAGCGCGTTGCTGAAAACACACGAGCAGCAGATCAGGAAATCGAGCTTT	3264
Db	8089	AGGCCAAGCAGCGCGCGTTGCTGAAAACACACGAGCAGCAGATCAGGAAATCGAGCTTT	8148
Qy	3265	CCTTGTTCGATATTTGCGCGTGGCGACACGATGCGAGCGATGCGCAAAACGACGCGCC	3324
Db	8149	CCTTGTTCGATATTTGCGCGTGGCGACACGATGCGAGCGATGCGCAAAACGACGCGCC	8208
Qy	3325	GCTCTCCCTGTTTACACGCGCAACAAGAAAATTCGCGCGAGGCGCTCGAAAAAAGG	3384
Db	8209	GCTCTCCCTGTTTACACGCGCAACAAGAAAATTCGCGCGAGGCGCTCGAAAAAAGG	8268
Qy	3385	TCATTTTCCACGTCACAAAGGAGCTGAAGTACCTTACACCGGCGTGCAGCTCGGCGCG	3444
Db	8269	TCATTTTCCACGTCACAAAGGAGCTGAAGTACCTTACACCGGCGTGCAGCTCGGCGCG	8328
Qy	3445	ACGATGACAACTGGTGTGGCAGCAGCTGTGGAGTACGCAAGCGCACCCCTATCGGCG	3504
Db	8329	ACGATGACAACTGGTGTGGCAGCAGCTGTGGAGTACGCAAGCGCACCCCTATCGGCG	8388
Qy	3505	AGCCGATCACCTTTCAGCTTCTACGAGCTTTGCCAGGACCTGGGCTGGTCCGATCAATGGCC	3564

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Db      8389  AGCGATCACTTTCACGTTCTACGAGCTTTCAGGACCTGGGCTGCTGATCAATGGCC 8448
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Db      8449  GGTATTACAGAGGCGAGGAATGCTGTGCGCCCTACAGGCGACGGCGATGGCTTCA 8508
Qy      3625  CGTCCGACCGGTTGGGCACTGGAATCGGTGTCGCTGCTGCAACCGCTTCGCGCTCTGG 3684
Db      8509  CGTCCGACCGGTTGGGCACTGGAATCGGTGTCGCTGCTGCAACCGCTTCGCGCTCTGG 8568
Qy      3685  ACCGTGGCAAGAAACGTCGCGTTGCCAGGTCCCTGATCGACGAGGAAATCGTCGTCTGT 3744
Db      8569  ACCGTGGCAAGAAACGTCGCGTTGCCAGGTCCCTGATCGACGAGGAAATCGTCGTCTGT 8628
Qy      3745  TTGCTGGCGACCACTACACGAAATTCATATGGGAGAGTACCGCAAGCTGTCGCGACGG 3804
Db      8629  TTGCTGGCGACCACTACACGAAATTCATATGGGAGAGTACCGCAAGCTGTCGCGACGG 8688
Qy      3805  CCGACCGATGTTTCGACTATTTTCAGCTCGCACCGGAGCGGTACCCGCTCAAGCTGGAAA 3864
Db      8689  CCGACCGATGTTTCGACTATTTTCAGCTCGCACCGGAGCGGTACCCGCTCAAGCTGGAAA 8748
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Db      8749  CTTTCCGCTCATGTCGGGATCGGATTCACCCCGCTGAAGAGTGGCGCGAGCAGTCG 8808
Qy      3925  GCGAAGCTCGGAAGAGTTGCGAGCGACGCGCCCTGGTGGAAACAGCCCTGGGTCAATG 3984
Db      8809  GCGAAGCTCGGAAGAGTTGCGAGCGACGCGCCCTGGTGGAAACAGCCCTGGGTCAATG 8868
Qy      3985  ACCTGGTGCAATGCAACGCTAGGCGCTTGGGGTCAAGTTCCGCGTGGGGTTCAGCAG 4044
Db      8869  ACCTGGTGCAATGCAACGCTAGGCGCTTGGGGTCAAGTTCCGCGTGGGGTTCAGCAG 8928
Qy      4045  CCAGCGCTTTACTGGCATTTTC 4065
Db      8929  CCAGCGCTTTACTGGCATTTTC 8949

RESULT 3
US-10-074-279-10
; Sequence 10, Application US/10074279
; Patent No. 6646184
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

Query Match      52.5%; Score 2522.2; DB 4; Length 13737;
Best Local Similarity 76.5%; Pred. No. 0;
Matches 3505; Conservative
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Db      4431  AAACGCGTTCGAAAGCGTGTGCGAGACACCGCGCGCGCGCGCGGCTGTGATACCTC 4490
Qy      117   GCGGAAAACTTGGCCCTCACTGACAGATGAGGGGCGGACGTTGACACTTTGAGGGCGGAC 176
Db      4491  GCGGAAAACTTGGCCCTCACTGACAGATGAGGGGCGGACGTTGACACTTTGAGGGCGGAC 4550
Qy      177   TCACCCGCGCGCGCTGTGACAGATGAGGGGCGAGCTCGATTTTCGCGCGCGGACGTCGTGAGC 236
Db      4551  TCACCCGCGCGCGCTGTGACAGATGAGGGGCGAGCTCGATTTTCGCGCGCGGACGTCGTGAGC 4610
Qy      237   TGCGCAGCTTCGAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCACAGATGATG 296
Db      4611  TGCGCAGCTTCGAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCACAGATGATG 4670
Qy      297   TGACCAAGCCTGGGGATAGTGCCCTGCGGTATTGACACTTTGAGGGGCGGACCTACTTGAC 356
Db      4671  TGACCAAGCCTGGGGATAGTGCCCTGCGGTATTGACACTTTGAGGGGCGGACCTACTTGAC 4730
Qy      357   AGATGAGGGCGCGATTCCTTGAACACTTGAGGGGCGAGTCTGCTGACAGATGAGGGGCGGAC 416
Db      4731  AGATGAGGGCGCGATTCCTTGAACACTTGAGGGGCGAGTCTGCTGACAGATGAGGGGCGGAC 4790
Qy      417   CTATTGACATTTGAGGGGCTGCCACAGGCGAGAAATCCAGCATTTGCAAGGGTTTCCGC 476
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Qy      477   CCGTTTTTCGCGCACCGCTAACCTGCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTTAACT 536
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Db      4971  CCGCTTCTCGAACCCCTCCCGCGCGCTAACCGGGGCTCCCATCCCCCAGGGGCTGCG 5030
Qy      619   -----AAAGTATGCGGTGTGAAATACCGCACAGAT 649
Db      5031  CCGCTCGCGCGGAAACGGCCCTACCCCAAAATGGCAGCGCTGGCAGTCTCTTGCCATTGC 5090
Qy      650   GCGTAAGGAGAAATACCGCATCAGGGCGTCTTCGCGTCTCTCGCTCACTGACTCGGTGC 709
Db      5091  CCGGATCGGGCGAGTAACGGGATGGCGCATCAGCCCGAGCGCGACCGCCGGAAGCATTTGA 5150
Qy      710   GCTCGGTGTTGCGCTCGCGGAGCGGTATCAGTCACTCAAGGGCGGTAAATACGGTTAT 769
Db      5151  CGTGCCGCGAGTGTGGCATTCGACATTCAGCGACACAGTTCGCGGGCAGTAGGGCGGCGG 5210
Qy      770   CC----- 771
Db      5211  CCTGGGTGGCGGCTGCGCTTCACTTCGCGCGTGGGGCATTCACGGACTTCATGGCGGG 5270
Qy      772   ----- 771
Db      5271  GCCGCAATTTTACCTTGGGCATTTCTTGGCATAGTGGTCCGCGGTCGCGTCTGCTGTT 5330
Qy      772   -----ACAGATCAGGGGATACGCGAGGAAAGAACATGTGAG 808
Db      5331  CGGGGTGCGATAAACCCAGCAACCATTTGAGGTGATAGTTATACCGAGGTAT 5390
Qy      809   CAAAAGG----- 815
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QY 816 -----CCAGCAAAAGGCCAGGAAACCGTAAAGAGCCGCTTCTGCTGGCGTTT 861  
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QY 862 TTCATAGGCTCCGC----- 876  
Db AGGCATAGGCGCGCTTATCAATATATCTATAGAAATGGCAAGCATAAACCTTGCA 5630  
QY 877 -----CCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGAGGTG 920  
Db TGGACTAATGCTTGAACCCAGGACATAACCTTATAGCTTGTAAATTTCTATCAATATG 5690  
QY 921 GCGAAACCCGACAG----- 934  
Db GGTAATGACTCCAACCTTATTTGATAGTGTATTTATGTTTCAGATAATGCCCGATGACTTTGTC 5750  
QY 935 -----GACTATAAAGTACCAGCGTTTCCCTCGGAAGCTCCCTGTCGCG 981  
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QY 982 TCTCCTGTTCCGACCCCTGCGCT-TACCGGATACCTGTGCGCTTTCTCCCTTCGGGAAG 1040  
Db CCTCAGATTGAGTTATGCGCTCAATTGCTGGGTATATCGCTTGTGATTAAGTGCAG 5870  
QY 1041 CGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTGCCTC 1100  
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QY 1446 AAGGATTTCAAGGGGCAAGGCATPAGGAGCGC----- 1477  
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QY 1478 -----GCTTATCAATATATCTATAGAAATGGCAAGCATAAACCTT-----GCATGGAC 1527  
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Db CATTCGCTTCTCGTCCGTCGATCAGGAGGATATCGGGGAAGAACAGTATGTCAGCT 7368  
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Qy 3505 AGCCGATCACCTTCACGTTCTACGAGCTTTGCCAGGACCTGGGCTGCTCGATCAATGGCC 3564  
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Qy 3565 GGTATTACGAAGCCGAGGAATTCCTGTGCGCCCTACAGGCGACGCGATGGGCTTCA 3624  
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Qy 3745 TTGCTGGCGACCACTACAGAAATTCATATATGGGAGAGTACCGAAGCTGTCGCCGACGG 3804  
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Db 8689 CCCGACGAGTGTTCGACTATTTAGCTCGCAACGGGAGCCGTACCCGCTCAAGCTGAA 8748  
Qy 3865 CTTTCCGCTCATGTGGGATCGGATTCACCCCGCTGGAAGAGTGGCGCGAGCAGGTTCG 3924

Db 8749 CTTTCGCTCATGTGCGGATCGGATTCACCCGCTGAAGAAGTGGCGAGCAGGTTCG 8808  
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RESULT 4  
US-09-280-428A-11/c  
; Sequence 11, Application US/09280428A  
; Patent No. 6495738  
; GENERAL INFORMATION:  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J  
; TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by  
; FILE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase  
; FILE REFERENCE: 50612  
; CURRENT APPLICATION NUMBER: US/09/280,428A  
; CURRENT FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: 60/079840  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 10323  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pDAB1542  
US-09-280-428A-11

Query Match 29.0%; Score 1393; DB 4; Length 10323;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1405; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 2641 CCAGGCCACCGCAAGTATTTGGGCAAGGGTTCGCTGCTGATTCGTCAGGCAAGATTC 2700  
Db 8900 CCATGCGCTCCATCAAGAAGAGCGACTTCGCGAGCTGGTATTCGTGAGGCAAGATTC 8841  
Qy 2701 GGAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTTGCCGATA 2760  
Db 8840 GGAATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTTGCCGATA 8781  
Qy 2761 AGTGTGATTAATCTGGACACCAAGGACACGAGCGGGTCAATATCAGGAATAAGGGCACATTG 2820  
Db 8780 AGTGTGATTAATCTGGACACCAAGGACACGAGCGGGTCAATATCAGGAATAAGGGCACATTG 8721  
Qy 2821 CCCCGCGCTGAGTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGACGCTTTGACCGGA 2880  
Db 8720 CCCCGCGCTGAGTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGACGCTTTGACCGGA 8661  
Qy 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCGCGCGAGGATGCCGAAACCATCG 2940  
Db 8660 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCGCGCGAGGATGCCGAAACCATCG 8601  
Qy 2941 CAAGCGGACCGCTCATGCTGCGCGCGGCAAACTTCAGTCCGCTCGGTTCGATGCTCC 3000  
Db 8600 CAAGCGGACCGCTCATGCTGCGCGCGGCAAACTTCAGTCCGCTCGGTTCGATGCTCC 8541  
Qy 3001 AGCAAGTACGCGCAAGATCGAGCGGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG 3060  
Db 8540 AGCAAGTACGCGCAAGATCGAGCGGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG 8481  
Qy 3061 CGCCATCGCGCGCGCTGGAGCTTCGCGTTCGATTCGAAACAGGAGGCGGAGGTTTGGCA 3120



Db 6272 AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCGCGGAGGATGCCGAACCATCG 6213  
Qy 2941 CAAGCCGACCGTCATCGTGTGCGCCCGCGAAACCTTCCAGTCCGTGCGTCCATGTTCC 3000  
Db 6212 CAAGCCGACCGTCATCGTGTGCGCCCGCGAAACCTTCCAGTCCGTGCGTCCATGTTCC 6153  
Qy 3001 AGCAAGCTACGGCCAGATCGAGCGGACAGCGTGCACCTGGCTCCCGCTGCCCTGCCCG 3060  
Db 6152 AGCAAGCTACGGCCAGATCGAGCGGACAGCGTGCACCTGGCTCCCGCTGCCCTGCCCG 6093  
Qy 3061 CGCCATCGCGCGCGTGTGAGCGTTTCCGCTGCTCTCGAACAGGAGCGGCGAGTTTGGCGA 3120  
Db 6092 CGCCATCGCGCGCGTGTGAGCGTTTCCGCTGCTCTCGAACAGGAGCGGCGAGTTTGGCGA 6033  
Qy 3121 AGTCGATGACATCGACACCGGAGAACTATGAGGACCAAGACGAAACCGCGCGCG 3180  
Db 6032 AGTCGATGACATCGACACCGGAGAACTATGAGGACCAAGACGAAACCGCGCGCG 5973  
Qy 3181 AGGACCTGGCAAAACAGGTGAGCGAGGCCAAGCAGGCGCGTGTGCTGAAACACACGAAGC 3240  
Db 5972 AGGACCTGGCAAAACAGGTGAGCGAGGCCAAGCAGGCGCGTGTGCTGAAACACACGAAGC 5913  
Qy 3241 AGCAGATCAAGGAAATCAGCTTTCCTTGTTCGATATTGCGCGCTGCGCGACACGATGC 3300  
Db 5912 AGCAGATCAAGGAAATCAGCTTTCCTTGTTCGATATTGCGCGCTGCGCGACACGATGC 5853  
Qy 3301 GAGCGATGCCAAACGACACCGGCGCGCTCTGCGCTGTTTCAACGCGCAACAAAGAAATCC 3360  
Db 5852 GAGCGATGCCAAACGACACCGGCGCGCTCTGCGCTGTTTCAACGCGCAACAAAGAAATCC 5793  
Qy 3361 CGCGGAGGCGCTGCAAAACAAGTCAATTTTCCACGTCACAAAGGACGTGAAGATCACCT 3420  
Db 5792 CGCGGAGGCGCTGCAAAACAAGTCAATTTTCCACGTCACAAAGGACGTGAAGATCACCT 5733  
Qy 3421 ACACCGCGCTCGAGCTCGCGGCCGACGATACGAACTGGTGTGCGACGAGTGTGAGT 3480  
Db 5732 ACACCGCGCTCGAGCTCGCGGCCGACGATACGAACTGGTGTGCGACGAGTGTGAGT 5673  
Qy 3481 ACGGAAGCGGACCCCTATCGCGAGCGGATCACCTTCACTGTTTACGAGTTTGCAGG 3540  
Db 5672 ACGGAAGCGGACCCCTATCGCGAGCGGATCACCTTCACTGTTTACGAGTTTGCAGG 5613  
Qy 3541 ACCTGGGCTGTGATCAATGGCGGTATTACAGAAAGCGGAGAAATGCTGTGCGGCC 3600  
Db 5612 ACCTGGGCTGTGATCAATGGCGGTATTACAGAAAGCGGAGAAATGCTGTGCGGCC 5553  
Qy 3601 TACAGCGACGGCGATGGGCTTTCAGTCCGACCGCGTTGGGCACCTTGAATTCGTTGTCG 3660  
Db 5552 TACAGCGACGGCGATGGGCTTTCAGTCCGACCGCGTTGGGCACCTTGAATTCGTTGTCG 5493  
Qy 3661 TGCTGACCGGTTCCGCGTCTGACCGGTGGCAAGAAACGTCCCGTTGCGAGTCTGTA 3720  
Db 5492 TGCTGACCGGTTCCGCGTCTGACCGGTGGCAAGAAACGTCCCGTTGCGAGTCTGTA 5433  
Qy 3721 TCGACGAGGAAATCGTGTGCTGTTTGTGCGACCACTACACGAAATTCATATGGGAGA 3780  
Db 5432 TCGACGAGGAAATCGTGTGCTGTTTGTGCGACCACTACACGAAATTCATATGGGAGA 5373  
Qy 3781 AGTACCGCAAGCTGTCCCGACCGCGGACGGATGTTTCGACTATTTTCAGCTTCGACCGGG 3840  
Db 5372 AGTACCGCAAGCTGTCCCGACCGCGGACGGATGTTTCGACTATTTTCAGCTTCGACCGGG 5313  
Qy 3841 AGCGTACCGCTCAAGCTGGAACCTTTCGCCCTCATGTGCGGATTCGATTCACCGCGG 3900  
Db 5312 AGCGTACCGCTCAAGCTGGAACCTTTCGCCCTCATGTGCGGATTCGATTCACCGCGG 5253  
Qy 3901 TGAAGAGTGGCGGACGAGTTCGCGAGCGCTCGAGAGTTCGAGGAGCGGCGCTGG 3960  
Db 5252 TGAAGAGTGGCGGACGAGTTCGCGAGCGCTCGAGAGTTCGAGGAGCGGCGCTGG 5193  
Qy 3961 TGAAGAGTGGCGGATCAATGATACCTGTGTGATTCGAAACGCTAGGCGCTTGTGGGGT 4020

Db 5192 TGGAACACACGCTGGGTCAATGATGACCTGTGTGCAATGCAACGCTAGGCGCTTGTGGGGT 5133  
Qy 4021 CAGTTCGCGCTGGGGTTTCAGCAGCGAGCGCTTTACTGGCATTTTC 4065  
Db 5132 CAGTTCGCGCTGGGGTTTCAGCAGCGAGCGCTTTACTGGCATTTTC 5088  
RESULT 6  
US-08-992-801-1/c  
; Sequence 1, Application US/08992801  
; Patent No. 6107544  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric  
; APPLICANT: Delaney, Terry  
; APPLICANT: Lawton, Kay  
; APPLICANT: Weymann, Kris  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Maleck, Klaus  
; TITLE OF INVENTION: Method For Breeding Disease Resistance  
; TITLE OF INVENTION: Into Plants  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6107544artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/992,801  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: US 08/648,949  
; APPLICATION NUMBER:  
; FILING DATE: 16-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,248  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,285  
; FILING DATE: 08-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14113 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "PR-1/luc construct"  
; US-08-992-801-1  
Query Match 29.0%; Score 1393; DB 3; Length 14113;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1405; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 2641 CCAGAGCCCAACGCAAGTATTTGGGCAAGGGTTCGCTGTTATTCGTGCGAGGCAAGATTC 2700  
Db 6512 CCATGCGCTCCATCAAGAAAGCGGACTTCGCGAGCTGTGTTATTCGTGCGAGGCAAGATTC 6453



QY 2701 GGAATACCAAGTACGAGAGGACGGCCAGACGGTCTTACGGGACCGACTTCATTGCGCGATA 2760  
DB 6452 GGAATACCAAGTACGAGAGGACGGCCAGACGGTCTTACGGGACCGACTTCATTGCGCGATA 6393  
QY 2761 AGGTGGATTATCTGGACACCAAGGACCGGCGGCTCAATCAGGAATAGGGCACAATTG 2820  
DB 6392 AGGTGGATTATCTGGACACCAAGGACCGGCGGCTCAATCAGGAATAGGGCACAATTG 6333  
QY 2821 CCCCGCGTGGTGGGCGCAATCCCGCAAGGAGGGTGAATGAATCGGACGCTTTTGACCGGA 2880  
DB 6332 CCCCGCGTGGTGGGCGCAATCCCGCAAGGAGGGTGAATGAATCGGACGCTTTTGACCGGA 6273  
QY 2881 AGGCATACAGGCAAGCACTGATCGACGCGGGTTTTCGCGCGAGGATGCGCAAAACCATCG 2940  
DB 6272 AGGCATACAGGCAAGCACTGATCGACGCGGGTTTTCGCGCGAGGATGCGCAAAACCATCG 6213  
QY 2941 CRAAGCGCACCGTCATCGCTGCGCCCGCGAAGACCTTCCAGTCCGTCGGTCCGATGGTCC 3000  
DB 6212 CRAAGCGCACCGTCATCGCTGCGCCCGCGAAGACCTTCCAGTCCGTCGGTCCGATGGTCC 6153  
QY 3001 AGCAAGCTACGGCAAGATCGAGCGGACAGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG 3060  
DB 6152 AGCAAGCTACGGCAAGATCGAGCGGACAGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG 6093  
QY 3061 CGCCATCGGCGCGCTGGAGCGTTTCGCTGCTCTCGAACAAGGAGCGGCGAGTTTGGCGA 3120  
DB 6092 CGCCATCGGCGCGCTGGAGCGTTTCGCTGCTCTCGAACAAGGAGCGGCGAGTTTGGCGA 6033  
QY 3121 AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGAACGAAACCGCGCGG 3180  
DB 6032 AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGAACGAAACCGCGCGG 5973  
QY 3181 AGGACCTGGCAAAACAGGTGAGCGGCGCAAGCGCGGTTGCTGAAACACACGAAGC 3240  
DB 5972 AGGACCTGGCAAAACAGGTGAGCGGCGCAAGCGGCGGTTGCTGAAACACACGAAGC 5913  
QY 3241 AGCAGATCAAGAGAAATGCACTTTCCTTGTTCGATATGCGCGTGGCGCGACACGATGC 3300  
DB 5912 AGCAGATCAAGAGAAATGCACTTTCCTTGTTCGATATGCGCGTGGCGCGACACGATGC 5853  
QY 3301 GAGCGATGCCAAACGACACGGCCCGCTTGCCTCTGTTCCACCGCGCAACAGAAATCC 3360  
DB 5852 GAGCGATGCCAAACGACACGGCCCGCTTGCCTCTGTTCCACCGCGCAACAGAAATCC 5793  
QY 3361 CGCGGAGGCGCTGCAAAACAAGTCTATTTCCACGTCAACAGGACGTTGAAGTACACCT 3420  
DB 5792 CGCGGAGGCGCTGCAAAACAAGTCTATTTCCACGTCAACAGGACGTTGAAGTACACCT 5733  
QY 3421 ACACCGGCGTCAAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTTTGGAGT 3480  
DB 5732 ACACCGGCGTCAAGCTGCGGGCGGACGATGACGAACTGGTGTGGCAGCAGGTTTGGAGT 5673  
QY 3481 ACAGGAGGCGCACCTTATCGGCGAGCGGATCACCTTTCAGTTCTACGAGCTTTGCCAGG 3540  
DB 5672 ACAGGAGGCGCACCTTATCGGCGAGCGGATCACCTTTCAGTTCTACGAGCTTTGCCAGG 5613  
QY 3541 ACCTGGGCTGGTCAATCAATGGCCGCTATTACAGGAAGCGGAGGAACTGCTGTCGCGCC 3600  
DB 5612 ACCTGGGCTGGTCAATCAATGGCCGCTATTACAGGAAGCGGAGGAACTGCTGTCGCGCC 5553  
QY 3601 TACAGCGCAGCGGATGGGCTTTCAGCTCCGACCGCGTTGGCACCTTGGAACTCGGTGTCG 3660  
DB 5552 TACAGCGCAGCGGATGGGCTTTCAGCTCCGACCGCGTTGGCACCTTGGAACTCGGTGTCG 5493  
QY 3661 TGTGTACCGCTTCCGCGCTGCTGGACCGGTGGCAAGAAACGTCCTCCGTTGCGCAGGTCCTGA 3720  
DB 5492 TGTGTACCGCTTCCGCGCTGCTGGACCGGTGGCAAGAAACGTCCTCCGTTGCGCAGGTCCTGA 5433  
QY 3721 TCGACGAGGAATCGCTGCTGCTGTTGCTGGGACCACTACACGAATTCATATGGGAGA 3780  
DB 5432 TCGACGAGGAATCGCTGCTGCTGTTGCTGGGACCACTACACGAATTCATATGGGAGA 5373  
QY 3781 AGTACCGCAAGCTGTGCGCGACGGGCCCGAGCGGATGTTTCGACTATTTTCAGTCTCGACCGGG 3840

DB 5372 AGTACCGCAAGCTGTGCGCGACGGGCCGACGGATGTTTCGACTATTTTCAGTCTCGACCGGG 5313  
QY 3841 AGCCGTACCGCTCAAGCTTGGAAACCTTCCGCTCATGTCCGATCGGATTCACCCGG 3900  
DB 5312 AGCCGTACCGCTCAAGCTTGGAAACCTTCCGCTCATGTCCGATCGGATTCACCCGG 5253  
QY 3901 TGAAGAAGTGGCGCGACGAGCGTGGCGAAGCCCTGCGAAGAGTTTGCAGGCGAGCGGCTGG 3960  
DB 5252 TGAAGAAGTGGCGCGACGAGCGTGGCGAAGCCCTGCGAAGAGTTTGCAGGCGAGCGGCTGG 5193  
QY 3961 TGAACACACGCTGGGTCATATGATGACCTTGGTGCATTTGCAAAACGCTAGGGCTTTGTGGGT 4020  
DB 5192 TGAACACACGCTGGGTCATATGATGACCTTGGTGCATTTGCAAAACGCTAGGGCTTTGTGGGT 5133  
QY 4021 CAGTTCCGCTGGGGTTTCAGGACCGCGCTTTTACTGGCATTTTC 4065  
DB 5132 CAGTTCCGCTGGGGTTTCAGGACCGCGCTTTTACTGGCATTTTC 5088

RESULT 7  
US-09-223-535-1/c  
; Sequence 1, Application US/09223535  
; Patent No. 6232525  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric  
; APPLICANT: Delaney, Terry  
; APPLICANT: Lawton, Kay  
; APPLICANT: Weymann, Kris  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Maleck, Klaus  
; TITLE OF INVENTION: Method For Breeding Disease Resistance  
; TITLE OF INVENTION: Into Plants  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6232525artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/223,535  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/992,801  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/165,248  
; FILING DATE: 10-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,285  
; FILING DATE: 08-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14113 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single





Db	421	GGCTGGAGCAATCTGCTCATGTGTGAGCGCGATGGCGTCTTTCCTCGGAAGAGTATGAA	480
Qy	2075	GATGAACAAAGCCCTGAAAGATTATCGAGCTGTATCGCGAGTGCATCAGGCTCTTTTCAC	2134
Db	481	GATGAACAAAGCCCTGAAAGATTATCGAGCTGTATCGCGAGTGCATCAGGCTCTTTTCAC	540
Qy	2135	TCCATCGACATATCGGATTCTCCCTATACGAATAGCTTAGCAGCGCTTAGCGGAATTG	2194
Db	541	TCCATCGACATATCGGATTCTCCCTATACGAATAGCTTAGCAGCGCTTAGCGGAATTG	600
Qy	2195	GATTACTTACTGAATAACGATCTGGCCGATGTGGATTGCGAAACTGGGAAGAAGACACT	2254
Db	601	GATTACTTACTGAATAACGATCTGGCCGATGTGGATTGCGAAACTGGGAAGAAGACACT	660
Qy	2255	CCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGCCCGAAGAGGAA	2314
Db	661	CCATTTAAAGATCCGCGAGCTGTATGATTTTTTAAAGACGGAAGCCCGAAGAGGAA	720
Qy	2315	CTTGTCTTTTCCACCGCGACCTGGGAGACAGCAACATCTTGTGAAAGATGCCAAAGTA	2374
Db	721	CTTGTCTTTTCCACCGCGACCTGGGAGACAGCAACATCTTGTGAAAGATGCCAAAGTA	780
Qy	2375	AGTGGCTTTTATGATCTTGGAGAAAGCGGAGCGGACCAAGTGTATGACATTTGCCCTTC	2434
Db	781	AGTGGCTTTTATGATCTTGGAGAAAGCGGAGCGGACCAAGTGTATGACATTTGCCCTTC	840
Qy	2435	TGCGTCCGCTCGATCAGGAGGATATCGGGAGAAACAGTATGTCGAGCTATTTTTTGAC	2494
Db	841	TGCGTCCGCTCGATCAGGAGGATATCGGGAGAAACAGTATGTCGAGCTATTTTTTGAC	900
Qy	2495	TTACTGGGGATCAAGCTGTATGGGAGAAATATAATTTTACTGGATGAATTG	2554
Db	901	TTACTGGGGATCAAGCTGTATGGGAGAAATATAATTTTACTGGATGAATTG	960
Qy	2555	TTTTTAGTACCTAGATGCGCGCAACGATGCCGGCGACAAGCAGGAGCGCACCGACTTCTT	2614
Db	961	TTTTTAGTACCTAGATGCGCGCAACGATGCCGGCGACAAGCAGGAGCGCACCGACTTCTT	1020
Qy	2615	CCGCATCAAGTGTGTTTGG	2632
Db	1021	CCGCAAAAGAGTCTAGG	1038

RESULT 10

US-09-171-517B-15  
; Sequence 15, Application US/09171517B  
; Patent No. 6355254  
; GENERAL INFORMATION:  
; APPLICANT: Finlay, B. Brett  
; APPLICANT: Kenny, Brendan  
; APPLICANT: Stein, Markus  
; TITLE OF INVENTION: PATHOGENIC ESCHERICHIA COLI ASSOCIATED PROTEIN  
; FILE REFERENCE: 07422/019001  
; CURRENT APPLICATION NUMBER: US/09/171,517B  
; CURRENT FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: PCT/CA97/00265  
; PRIOR FILING DATE: 1997-04-23  
; PRIOR APPLICATION NUMBER: 60/015,999  
; PRIOR FILING DATE: 1996-04-23  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 856  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-09-171-517B-15

Query Match 16.8%; Score 807; DB 4; Length 856;  
Best Local Similarity 99.4%; Pred. No. 1.9e-227;  
Matches 810; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1756 GAAATAATAATGCTAAATGAGATATACCGGAATTGAAAAAATCTGATCGAAAAATA 1815

Db	26	GGAGGAATAAATGGCTAAAATGAGATAATCACCGGAATTTGAAAAAACTGATCGAAAAATA	85
Qy	1816	CGCTCGCTAAAAGATACGGAAGGATGCTCTCTGCTAAGGTATATAAGCTGGTGGAGA	1875
Db	86	CGCTCGCTAAAAGATACGGAAGGATGCTCTCTGCTAAGGTATATAAGCTGGTGGAGA	145
Qy	1876	AAATGAAAAACCTATATTTTAAAAATGACGACAGCCGGTATAAAGGACCAACCTATGATGT	1935
Db	146	AAATGAAAAACCTATATTTTAAAAATGACGACAGCCGGTATAAAGGACCAACCTATGATGT	205
Qy	1936	GGAAACGGGAAAAAGGACATGATCTATGGCTGGAAGAAAAAGCTGCCTGTTCCTGCTTCCAAAGTCTCT	1995
Db	206	GGAAACGGGAAAAAGGACATGATCTATGGCTGGAAGAAAAAGCTGCCTGTTCCTGCTTCCAAAGTCTCT	265
Qy	1996	GCATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGATGAGCGCCGATGGCCCTCT	2055
Db	266	GCATTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGATGAGCGCCGATGGCCCTCT	325
Qy	2056	TTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTATCCAGCTGTATCGGA	2115
Db	326	TTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTATCCAGCTGTATCGGA	385
Qy	2116	GTGCATCAGGCTCTTTTCACTCCATCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGA	2175
Db	386	GTGCATCAGGCTCTTTTCACTCCATCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGA	445
Qy	2176	CAGCCCTTAGCGGAATTGGATTACTTACTGAATACGATCTGGCCGATGTGGATTGCGGA	2235
Db	446	CAGCCCTTAGCGGAATTGGATTACTTACTGAATACGATCTGGCCGATGTGGATTGCGGA	505
Qy	2236	AAACTCGGAAGAGACACTCCATTTTAAAGATCCGCGGAGCTGTATGATTTTTTAAAGAC	2295
Db	506	AAACTCGGAAGAGACACTCCATTTTAAAGATCCGCGGAGCTGTATGATTTTTTAAAGAC	565
Qy	2296	GGAAAAAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACCTGGGAGACAGCAACATCTT	2355
Db	566	GGAAAAAGCCGGAAGAGAACTTGTCTTTTCCACGGCGACCTGGGAGACAGCAACATCTT	625
Qy	2356	TGTGAAAGATGGCAAAAGTAAAGTGGCTTTTATGATCTTGGAGAGCGGCGGCGGACAA	2415
Db	626	TGTGAAAGATGGCAAAAGTAAAGTGGCTTTTATGATCTTGGAGAGCGGCGGCGGACAA	685
Qy	2416	GTGCTATGACATGCTTCTGCGTCCGCTCGATCAGGAGGATATCGGGGAAGAACAGTA	2475
Db	686	GTGCTATGACATGCTTCTGCGTCCGCTCGATCAGGAGGATATCGGGGAAGAACAGTA	745
Qy	2476	TGTCGAGCTATTTTTTACCTTACTGGGATCAAGCTGTATGGGAAAAATAAAATATTA	2535
Db	746	TGTCGAGCTATTTTTTACCTTACTGGGATCAAGCTGTATGGGAAAAATAAAATATTA	805
Qy	2536	TATTTTACTGGGATGAATTGTTTAGTACCTAGATG	2570
Db	806	TATTTTACTGGGATGAATTGTTTAGTACCTGGAGG	840

RESULT 11

US-09-134-000C-3304  
; Sequence 3304, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3304  
; LENGTH: 795

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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-3304

Query Match      16.5%; Score 795; DB 4; Length 795;
Best Local Similarity 100.0%; Pred. No. 6.2e-224; Mismatches 0; Indels 0; Gaps 0;
Matches 795; Conservative 0;

QY 1766 ATGGCTAAATGAGATATACCGGAATTGAAAGAACTGATCGAAATAATACCGCTCGGTA 1825
DB 1 ATGGCTAAATGAGATATACCGGAATTGAAAGAACTGATCGAAATAATACCGCTCGGTA 60

QY 1826 AAAGATACGGAAGGATGCTCTCTGTAAGGTATATAAGCTGTGGGAGAAATGAAAC 1885
DB 61 AAAGATACGGAAGGATGCTCTCTGTAAGGTATATAAGCTGTGGGAGAAATGAAAC 120

QY 1886 CTATATTTAAATATGAGACAGCGATATAGAGGACCACTATGATGGAACGGGA 1945
DB 121 CTATATTTAAATATGAGACAGCGATATAGAGGACCACTATGATGGAACGGGA 180

QY 1946 AAGGACATGATGCTATGGCTGGAAGAAAGCTGCTGTTCCAAAGGTCTTGCACTTTGAA 2005
DB 181 AAGGACATGATGCTATGGCTGGAAGAAAGCTGCTGTTCCAAAGGTCTTGCACTTTGAA 240

QY 2006 CGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGCGCTCTTTGCTCGAA 2065
DB 241 CGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGCGCGATGCGCTCTTTGCTCGAA 300

QY 2066 GAGTATGAAGTAAAGCAATCTGCTCATGAGTGAGCGCGATGCGCTCTTTGCTCGAA 2125
DB 301 GAGTATGAAGTAAAGCAATCTGCTCATGAGTGAGCGCGATGCGCTCTTTGCTCGAA 360

QY 2126 CTCTTTCACTTCCATCGACATATCGGATGTCCTTATACGAATAGCTTAGACAGCCGCTTA 2185
DB 361 CTCTTTCACTTCCATCGACATATCGGATGTCCTTATACGAATAGCTTAGACAGCCGCTTA 420

QY 2186 GCCGAATTTGATTTACTTGAATAACGATCTGGCCGATGTGGATTTGCGAAACTCGGAA 2245
DB 421 GCCGAATTTGATTTACTTGAATAACGATCTGGCCGATGTGGATTTGCGAAACTCGGAA 480

QY 2246 GAAGACATCCATTTAAAGATCCGCGAGCTGTATGATTTTAAAGACGGAAGCC 2305
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QY 2306 GAAGAGCAATCTGCTTTTCCACGCGACCTGGGAGACGAAACATCTTTGTGAAGAT 2365
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QY 2366 GCGAAAGTAAAGTGGCTTTTATGATCTTGGGAGAAAGCGGACGAGCGCAAGTGGTATGAC 2425
DB 601 GCGAAAGTAAAGTGGCTTTTATGATCTTGGGAGAAAGCGGACGAGCGCAAGTGGTATGAC 660

QY 2426 ATTGCTTCTGCTCGGCTCGATCAGGAGGATATCGGGAAGAACAGTATGTCGAGCTA 2485
DB 661 ATTGCTTCTGCTCGGCTCGATCAGGAGGATATCGGGAAGAACAGTATGTCGAGCTA 720

QY 2486 TTTTGTGACTTACTGGGGTCAAGCTGATTTGGGAGAAATAAATATTTATTTTACTG 2545
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QY 2546 GATGAATTTGTTAG 2560
DB 781 GATGAATTTGTTAG 795
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RESULT 12  
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; Sequence 11, Application US/09280428A  
; Patent No. 6495738  
; GENERAL INFORMATION:  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J  
; TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by

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; TITLE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase
; FILE REFERENCE: 50612
; CURRENT APPLICATION NUMBER: US/09/280,428A
; CURRENT FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/079840
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 10323
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pDAB1542
; US-09-280-428A-11
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Best Local Similarity 99.4%; Pred. No. 4.4e-171;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 9688 AAACGCCGTCGAAGCCGTCGTGCGAGACACCGCGGCGCGCGGCTTGTGATACCTCGCGG 9747

QY 121 AAACCTTGCCCTCACTGACAGATGAGGGCGGACGCTTGACACTTGAGGGCGGACTCAC 180
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DB 9808 CCGGCGCGCGCTTGACAGATGAGGGCGGACGCTGATTTTCGCGCGGCGACGCTGAGCTGGC 9867

QY 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
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QY 301 CAAAGCTGGGATAGTGCCTCGGCTGATGACACTTGAGGGCGGCGACTACTGACAGAT 360
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QY 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCACAGATTTTCCAAAGGTTTCCGCGCGT 480
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QY 601 CTTCTCGAACCTTCCCGGAAAGGTA 625
DB 10228 CTTCTCGAACCTTCCCGGCGGCTA 10252
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; Sequence 1, Application US/09223134  
; Patent No. 6057490  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John  
; APPLICANT: Uknes, Scott  
; APPLICANT: Ward, Eric

```

/ APPLICANT: Delaney, Terry
/ APPLICANT: Lawton, Kay
/ APPLICANT: Weymann, Kris
/ APPLICANT: Steiner, Henry-York
/ APPLICANT: Maleck, Klaus
/ TITLE OF INVENTION: Method For Breeding Disease Resistance
/ TITLE OF INVENTION: Into Plants
/ NUMBER OF SEQUENCES: 1
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 605749artis Corporation
/ STREET: 3054 Cornwallis Road
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/223,134
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/992,801
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/165,248
/ FILING DATE: 10-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/002,285
/ FILING DATE: 08-JAN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: CGC1673/CIP3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8587
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14113 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "PR-1/luc construct"
/
/ US-09-223-134-1
/
/ Query Match 12.9%; Score 618.6; DB 3; Length 14113;
/ Best Local Similarity 99.4%; Pred. No. 5.5e-171;
/ Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
/
Qy 1 CCGGGCTGGTTCCTCGCGCTGGCTGGCGGCGGCTATGGCCCTGCACACGGCCAG 60
Db 864 CCGGGCTGGTTCCTCGCGCTGGCTGGCGGCGGCTATGGCCCTGCACACGGCCAG 923
/
Qy 61 AAAGCCGTCGAAGCCGTGTCGAGACACCGCGCGCGGCTGTGGATACCTCGGG 120
Db 924 AAAGCCGTCGAAGCCGTGTCGAGACACCGCGCGCGGCTGTGGATACCTCGGG 983
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Qy 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGGAGGGCCGACTCAC 180
Db 984 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGGAGGGCCGACTCAC 1043
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Qy 181 CCGCGCGGGCTTACAGATGAGGGCGGCTTCGATTCGCGCGCGGACGTGGAGCTGGC 240
Db 1044 CCGCGCGGGCTTACAGATGAGGGCGGCTTCGATTCGCGCGCGGACGTGGAGCTGGC 1103
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Qy 241 CAGCCTCGAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 300
Db 1104 CAGCCTCGAAATCGGCGAAACCGCTGATTTTACGCGAGTTTCCACAGATGATGTGA 1163

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Qy 301 CAAGCCTGGGATAAGTGCCTGCGGTATTGACACTTGAGGGGCGCGCACTACTGACAGAT 360
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Qy 421 TGACATTTGAGGGGCTGTCCACAGGAGAAAATCCAGCAATTTTCAAGGGGTTTCCGCCCGT 480
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Qy 481 TTTTCGGCCACCGCTAACTGCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTTAACTGCTTTG 540
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Qy 601 CTTCTCGAAACCTTCCCGAAAGGTA 625
Db 1464 CTTCTCGAAACCTTCCCGCGCGCGCTA 1488
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; Sequence 1, Application US/08992801
; Patent No. 6107544
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Uknes, Scott
; APPLICANT: Ward, Eric
; APPLICANT: Delaney, Terry
; APPLICANT: Lawton, Kay
; APPLICANT: Weymann, Kris
; APPLICANT: Steiner, Henry-York
; APPLICANT: Maleck, Klaus
; TITLE OF INVENTION: Method For Breeding Disease Resistance
; TITLE OF INVENTION: Into Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6107544artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,801
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/648,949
; FILING DATE: 16-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,248
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,285
; FILING DATE: 08-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1673/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEPHONE: 919-541-8587

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; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PR-1/luc construct"
US-08-992-801-1

Query Match 12.9%; Score 618.6; DB 3; Length 14113;
Best Local Similarity 99.4%; Pred. No. 5.5e-171;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGGGCTGGTTGCCCTCGCCCTGGCGCTGGCGCGCGCTCTATGCGCCCTGCAAAACGCCGCCAG 60
DB 864 CCGGGCTGGTTGCCCTCGCCCTGGCGCTGGCGCGCGCTCTATGCGCCCTGCAAAACGCCGCCAG 923

QY 61 AAACGCCGTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGTGCGATACCTCGCGG 120
DB 924 AAACGCCGTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGTGCGATACCTCGCGG 983

QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGCGAGCTTGACACTTGAGGGCGCGACTCAC 180
DB 984 AAAAATTGGCCCTCACTGACAGATGAGGGCGCGAGCTTGACACTTGAGGGCGCGACTCAC 1043

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DB 1044 CCGGCGCGGCTGTGACAGATGAGGGCGAGCTCGATTTCCGCCGCGGCGAGCTGGAGCTGGC 1103

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DB 1104 CAGCCTCGCAAAATCGCGAAACGCCCTGATTTTACCGCGAGTTTCCACAGATGATGTGA 1163

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DB 1224 GAGGGCGCGATCTTGTACACTTTAGGGCGAGAGTCTGACAGATGAGGGCGCGACTCTAT 1283

QY 421 TGACATTTGAGGGCTGTCCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCCGCCCTG 480
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; APPLICANT: Ryals, John
; APPLICANT: Uknes, Scott
; APPLICANT: Ward, Eric
; APPLICANT: Delaney, Terry
; APPLICANT: Lawton, Kay
; APPLICANT: Weymann, Kris
; APPLICANT: Steiner, Henry-York
; APPLICANT: Maleck, Klaus
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; TITLE OF INVENTION: Method For Breeding Disease Resistance
; TITLE OF INVENTION: Into Plants
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6232525artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/223,535
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/992,801
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,248
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,285
; FILING DATE: 08-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CG1673/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PR-1/luc construct"
US-09-223-535-1
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Query Match 12.9%; Score 618.6; DB 3; Length 14113;
Best Local Similarity 99.4%; Pred. No. 5.5e-171;
Matches 621; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 AAACGCCGTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGTGCGATACCTCGCGG 120
DB 924 AAACGCCGTGGAAGCGCTGTGCGAGACACCGCGCGCGCGCTGTGCGATACCTCGCGG 983

QY 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGCGAGCTTGACACTTGAGGGCGCGACTCAC 180
DB 984 AAAAATTGGCCCTCACTGACAGATGAGGGCGCGAGCTTGACACTTGAGGGCGCGACTCAC 1043

QY 181 CCGGCGCGGCTGTGACAGATGAGGGCGAGCTCGATTTCCGCCGCGGCGAGCTGGAGCTGGC 240
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QY 241 CAGCCTCGCAAAATCGCGAAACGCCCTGATTTTACCGCGAGTTTCCACAGATGATGTGA 300
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QY 301 CAAAGCTGGGATAAGTGCCTCGCGTATGACACTTTGAGGGCGCGACTCTGACAGAT 360
DB 1164 CAAAGCTGGGATAAGTGCCTCGCGTATGACACTTTGAGGGCGCGACTCTGACAGAT 1223
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Db	1404	TTTTTAAACAGGGCTGCGCCCTGTGCGCGTGACCGCGCAGCGAGGGGGTGCCCCC	1463
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)

11960.100 Million cell updates/sec

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Perfect score: 4805

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Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 6382046

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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12	4531.4	94.3	6865	10	US-09-845-064-13
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16	4531.4	94.3	8654	10	US-09-845-064-14	Sequence 14, Appl	
17	4531.4	94.3	8987	10	US-09-845-064-22	Sequence 22, Appl	
18	4531.4	94.3	9143	10	US-09-845-064-12	Sequence 12, Appl	
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20	4531.4	94.3	9390	10	US-09-845-064-20	Sequence 20, Appl	
21	4528.2	94.2	8654	10	US-09-845-064-11	Sequence 11, Appl	
22	4528.2	94.2	9390	10	US-09-845-064-18	Sequence 18, Appl	
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40	2536.2	52.8	14446	9	US-09-810-861B-4	Sequence 4, Appl	
41	2536.2	52.8	15077	10	US-09-845-064-57	Sequence 57, Appl	
42	2536.2	52.8	15208	10	US-09-845-064-51	Sequence 51, Appl	
43	2536.2	52.8	15430	13	US-10-250-821-25	Sequence 25, Appl	
44	2536.2	52.8	15430	13	US-10-250-553-25	Sequence 25, Appl	
45	2536.2	52.8	17752	13	US-10-250-821-28	Sequence 28, Appl	

ALIGNMENTS

RESULT 1

US-09-845-064-10  
; Sequence 10, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 4805  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pmrt1191  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColeI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)

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; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
; OTHER INFORMATION: and P382, enabling the increase in the rate of
; OTHER INFORMATION: replication
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Ala1ine synthetase terminator
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4566)..(4625)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4625)..(4798)
; OTHER INFORMATION: T-DNA right border
; -09-845-064-10

Query Match      100.0%; Score 4805; DB 10; Length 4805;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4805; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGCTGGTGGCCCTCGCCGCTGGGCTGGGGCCGCTATGGCCCTGCAACCGCCGAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 AAACGCCGTGCAAGCCGTGTGCAGACACCGCGCCGCGCGTGTGGATACCTCGCGG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 AAACGCCGTGCAAGCCGTGTGCAGACACCGCGCCGCGCGTGTGGATACCTCGCGG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 AAAAATTGGCCCTCACTGCACAGATGAGGGCGGACGTGTGACACTTGAGGGCCGACATCAC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGACGCTGGAGCTGGC 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 241 CAGCCTCGCAAAATCGGGCAAAAACCCCTGATTTTACGCGAGTTTCCCAAGATGATGTGA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 301 CAAGCCTGGGGATAAAGTGCCTGCGGTATTGACACTTTGAGGGCGCGACTACTGACAGAT 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 361 GAGGGCGCGATCCTTGACACTTGAGGGCGAGTGTGACAGATGAGGGCGCGACCTAT 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 421 TGACATTTGAGGGCTGTGCACAGGCAAAATCCAGCATTTGCAAGGTTTCGCGCCGT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 481 TTTTCGCGCCACCGTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 541 TTTTAAACAGGGCTGGCCCTGTGCGGTGACCGCGCACCGCGAAGGGGGTCCCGCC 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 601 CTTCCTGAACCCCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 661 AAATACCGCATCAGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGGTGCTT 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 661 AAATACCGCATCAGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGGTGCTT 720
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Qy 721 CGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCA 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 721 CGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCA 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 781 GGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 840
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 841 AAGGCCGCTTGTCTGCGGTTTTTCCATAGGCTCCGCCCTTACGAGCATCAAAAT 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 901 CGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGGCTTTCCC 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 961 CTTGGAAGCTCCCTCGTGGCTCTCTCTGTTCGACCCCTCGCTTACCGGATACCTGTCC 1020
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1021 GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1081 TCGGTGTAGTCTCGCTCCAAAGCTGGGTGTGTCACGAACCCCGCTTCAGCCCGAC 1140
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1141 CGCTGGCCCTTATCCGGTAACTATCGTTGAGTCCAAACCCGGTCAAGACACGACTTATCG 1200
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1201 CCACTGGCAGCAGCTTCTACCATATCCCGATAAACCCGAGCAACCATTTTCAGGTGAT 1260
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1261 AGTTAAGATTATACCGAGGTATGAAAACGAGAAATGGACCTTTTACAGAAATTAATCTATGA 1320
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1321 AGCCCATATTTTAAAGCTTACCAAGCAGAGGATGAAGAGGATGAGAGGAGGAGATTG 1380
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1381 CTTTGAATATATTGACAACTACTGATAGATAATACATCTTTTATATAGAGATATCGCCG 1440
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1441 TATGTAAGATTTCAGGGGCAAGGATAGCGAGCGCTTATCAATATATCTATAGAAAT 1500
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1501 GGGCAAGCATATAAAACTTTCATGGAATATGCTTGAAACCCAGGACAAATAACCTTATAG 1560
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1561 CTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCCGTCGATCTATGTTATACG 1620
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1621 CCAACTTTGAAAAACACTTTTGAAGAAAGCTGTTTTCTGGTATTTTAAAGTTTATAGAAATGCAA 1680
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1681 GGAACAGTGAATTTGGAGTTTGGTCTTGTGTTAATAATAGCTTCTTGGGTATCTTTAAATACT 1740
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1741 GTAGAAAAGAGGAGGAAATAAATGCTTAAATAGAGATATACCCGGAATTTGAAAAA 1800
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1801 ACTGATCGAAAAATACCGCTGCGTAAAAAGATACGGAAGGAATGTCTCTCTAGGTATA 1860
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1801	Db	 ACTGATCGAANAATACCGCTGCGTAAAGATACGGAAGGAATGTCTCTCTTAAGGTATA	1860
1861	Qy	TAAGCTGGTGGGAGAAAATGAAAACCTTATTTTAAAAATGACGACAGCGGTATAAAGG	1920
1861	Db	TAAGCTGGTGGGAGAAAATGAAAACCTTATTTTAAAAATGACGACAGCGGTATAAAGG	1920
1921	Qy	GACCACCTATGATGTGGAACGGGAAAAGGACATGATCTATGGCTGGAAGAAAGCTGCC	1980
1921	Db	GACCACCTATGATGTGGAACGGGAAAAGGACATGATCTATGGCTGGAAGAAAGCTGCC	1980
1981	Qy	TGTTCCAAAGGTCTGTCACTTTGAAACGGCATGATGGCTGAGGCAATCTGCTCATGAGTGA	2040
1981	Db	TGTTCCAAAGGTCTGTCACTTTGAAACGGCATGATGGCTGAGGCAATCTGCTCATGAGTGA	2040
2041	Qy	GGCCGATGGCGTCTCTTGTCTCGAAGAGTATGAAGATGAACAAAGCCCTCGAAAAGATTAT	2100
2041	Db	GGCCGATGGCGTCTCTTGTCTCGAAGAGTATGAAGATGAACAAAGCCCTCGAAAAGATTAT	2100
2101	Qy	CGAGCTGATATCGCGAGTGCAATCAGGCTCTTTCACATCCATCGACATATCGGATTGTCCCTA	2160
2101	Db	CGAGCTGATATCGCGAGTGCAATCAGGCTCTTTCACATCCATCGACATATCGGATTGTCCCTA	2160
2161	Qy	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATACCATCTGGC	2220
2161	Db	TACGAATAGCTTAGACAGCGCTTAGCCGAATTTGGATTACTTACTGAAATACCATCTGGC	2220
2221	Qy	CGATGTCGATTTGCGAAAACCTGGGAAGAGACACTCCATTTTAAAGATCCGCGCAGCTGTA	2280
2221	Db	CGATGTCGATTTGCGAAAACCTGGGAAGAGACACTCCATTTTAAAGATCCGCGCAGCTGTA	2280
2281	Qy	TGATTTTTTAAAGACGGAAGCCGGAAGAGGAACCTTGTCTTTTCCACGCGCACCTGGG	2340
2281	Db	TGATTTTTTAAAGACGGAAGCCGGAAGAGGAACCTTGTCTTTTCCACGCGCACCTGGG	2340
2341	Qy	AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAAGTGGCTTTATTTGATCTTTGGGAAG	2400
2341	Db	AGACAGCAACATCTTTGTGAAAGATGCAAAAGTAAAGTGGCTTTATTTGATCTTTGGGAAG	2400
2401	Qy	CGGCAGGCGGCAACAAGTGTTATGACATGTCCTTCTGCTCCGCTCGATCAGGAGAGATAT	2460
2401	Db	CGGCAGGCGGCAACAAGTGTTATGACATGTCCTTCTGCTCCGCTCGATCAGGAGAGATAT	2460
2461	Qy	CGGGGAAGAACAGTATGTCGAGCTATTTTTTGACTTACTCGGGATCAAGCCTGATTGGGA	2520
2461	Db	CGGGGAAGAACAGTATGTCGAGCTATTTTTTGACTTACTCGGGATCAAGCCTGATTGGGA	2520
2521	Qy	GAAAAATAAATAATATATTTTACTGGAATGAATTTGTTTAGTACTAGATGTGGCAACG	2580
2521	Db	GAAAAATAAATAATATATTTTACTGGAATGAATTTGTTTAGTACTAGATGTGGCAACG	2580
2581	Qy	ATCCGCGCACAGCAGGAGCGACCACTTCTTCCGATCAAGTGTGTTTGGCTCTCAGG	2640
2581	Db	ATCCGCGCACAGCAGGAGCGACCACTTCTTCCGATCAAGTGTGTTTGGCTCTCAGG	2640
2641	Qy	CCGAGGCCACGGCAAGTATTTGGGCAAGGGGTGCTGGTATTTCTGCGAGCAAGTGTTCAGG	2700
2641	Db	CCGAGGCCACGGCAAGTATTTGGGCAAGGGGTGCTGGTATTTCTGCGAGCAAGTATTC	2700
2701	Qy	GGAATACCAAGTACAGAAAGGACGGCCAGACGGTCTACGGGAACGACTTCATTGCCGATA	2760
2701	Db	GGAATACCAAGTACAGAAAGGACGGCCAGACGGTCTACGGGAACGACTTCATTGCCGATA	2760
2761	Qy	AGGTGGATTATCTGGACCAAGCCACGGCGGTCAAAATCAGGATAGGGCACATTCG	2820
2761	Db	AGGTGGATTATCTGGACCAAGCCACGGCGGTCAAAATCAGGATAGGGCACATTCG	2820
2821	Qy	CCCCGGCGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGTTTGAACCGGA	2880
2821	Db	CCCCGGCGTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGTTTGAACCGGA	2880
2881	Qy	AGGCATACAGCAAGAACTGATCGACGCGGGTTTTCCCGCCGAGGATGCCGAACCATCG	2940

2881	Db	AGGCATACAGCGAAGAACTGATCGACGCGGGGTTTCCGCGGAGAGATGCCGAAACCAATCG	294
2941	Qy	CAAGCCGCAACCGTCATCGTGCGCCCGCGAAACCTTCCAGTCGGTCGGCTCGATGTTGCC	3000
2941	Db	CAAGCCGCAACCGTCATCGTGCGCCCGCGAAACCTTCCAGTCGGTCGGCTCGATGTTGCC	3000
3001	Qy	AGCAAGCTACGGGCAAGATCGAGCGGCAACAGCGTGCAACTGTGGCTCCCTTGCCTTGCCCG	3060
3001	Db	AGCAAGCTACGGGCAAGATCGAGCGGCAACAGCGTGCAACTGTGGCTCCCTTGCCTTGCCCG	3060
3061	Qy	CGCCATCGGCCCGGTGGAGCGTTCCGTCGTCTCGAACAAGGAGGGCGCAGGTTTGGCGA	3120
3061	Db	CGCCATCGGCCCGGTGGAGCGTTCCGTCGTCTCGAACAAGGAGGGCGCAGGTTTGGCGA	3120
3121	Qy	AGTCGATGACATCGACACGCGAGGAACATATGACGACCAAGAAAGCGAANAACCGCCGGCG	3180
3121	Db	AGTCGATGACATCGACACGCGAGGAACATATGACGACCAAGAAAGCGAANAACCGCCGGCG	3180
3181	Qy	AGGACCTTGGCAAAACAGGTCAGGAGCCCAAGCAGGCGCGGTTGCTTGAAACAACAGAAAC	3240
3181	Db	AGGACCTTGGCAAAACAGGTCAGGAGCCCAAGCAGGCGCGGTTGCTTGAAACAACAGAAAC	3240
3241	Qy	AGCAGATCAAGGAATGACAGCTTTCCTGTTTCATATTTGGCCGTCGCGGACACGATGC	3300
3241	Db	AGCAGATCAAGGAATGACAGCTTTCCTGTTTCATATTTGGCCGTCGCGGACACGATGC	3300
3301	Qy	GAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTTCCACGCGCAACAAGAAATCC	3360
3301	Db	GAGCGATGCCAAACGACACGCGCCGCTCTGCCCTGTTTCCACGCGCAACAAGAAATCC	3360
3361	Qy	CGCGGAGGCGCTTGCAAAACAAGGTCATTTTCCACGTCACAAAGGACGTGAAGATCACCT	3420
3361	Db	CGCGGAGGCGCTTGCAAAACAAGGTCATTTTCCACGTCACAAAGGACGTGAAGATCACCT	3420
3421	Qy	ACACCGCGTCGAGCTCGCGGCCGACGATGACGAACTGGTGTGGCAGCAGGTCTTGAGT	3480
3421	Db	ACACCGCGTCGAGCTCGCGGCCGACGATGACGAACTGGTGTGGCAGCAGGTCTTGAGT	3480
3481	Qy	ACGCGAAGCGCACCCCTATCGGCGAGCCGATCACCTTACGTTCTACGAGCTTGCCAGG	3540
3481	Db	ACGCGAAGCGCACCCCTATCGGCGAGCCGATCACCTTACGTTCTACGAGCTTGCCAGG	3540
3541	Qy	ACCTGGGCTGGTCGATCAATTGGCCGGTATTTACGAAAGGCCGAGGAATGCTGTCCGCC	3600
3541	Db	ACCTGGGCTGGTCGATCAATTGGCCGGTATTTACGAAAGGCCGAGGAATGCTGTCCGCC	3600
3601	Qy	TACAGCGGACGGCGATGGGCTTACGTCGACCGCGTTGGGCACTTGGATTCGGTGTCCG	3660
3601	Db	TACAGCGGACGGCGATGGGCTTACGTCGACCGCGTTGGGCACTTGGATTCGGTGTCCG	3660
3661	Qy	TGCTGCACCGCTTCCGGTCTCTGACCGTGGCAAGAAACGTCCTGGTGGCAGGTCTCTGA	3720
3661	Db	TGCTGCACCGCTTCCGGTCTCTGACCGTGGCAAGAAACGTCCTGGTGGCAGGTCTCTGA	3720
3721	Qy	TCGACGAGGAAATCGTCGTGCTTTGCTGGCGACCACTACACGAAATTCATATGGGAGA	3780
3721	Db	TCGACGAGGAAATCGTCGTGCTTTGCTGGCGACCACTACACGAAATTCATATGGGAGA	3780
3781	Qy	AGTACCGCAAGCTGTGCGCGACGGCCCGACCGATGTTTGCNACTATTTTTCAGCTCCGAC	3840
3781	Db	AGTACCGCAAGCTGTGCGCGACGGCCCGACCGATGTTTGCNACTATTTTTCAGCTCCGAC	3840
3841	Qy	AGCCGTACCCGCTCAAGCTTGGAACCTTCCGCCCTCATGTGCGGATCGGATTCACCCCGG	3900
3841	Db	AGCCGTACCCGCTCAAGCTTGGAACCTTCCGCCCTCATGTGCGGATCGGATTCACCCCGG	3900
3901	Qy	TGAAGAAGTGGCGGACGAGGTTCGCGAAGCCTTGCAGGAGTTTGCAGGACGCGGCTTG	3960
3901	Db	TGAAGAAGTGGCGGACGAGGTTCGCGAAGCCTTGCAGGAGTTTGCAGGACGCGGCTTG	3960
3961	Qy	TGGAACAACCGCTGGGTCAATGATGACTGGTGCAATTTGCAAAACGCTAGGGCTTGTGGGT	4020
3961	Db	TGGAACAACCGCTGGGTCAATGATGACTGGTGCAATTTGCAAAACGCTAGGGCTTGTGGGT	4020



Db 61 AAAGCGGTGTAAGCCGTGTGCAGACACCGCGCGCGCGCGGTGTGTGATACCTCGCGG 120  
Qy 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGGAGGGCGGACTCAC 180  
Db 121 AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGGAGGGCGGACTCAC 180  
Qy 181 CCGGCGGGGTTGACAGATGAGGGGAGGCTCGATTTCCGCGCGGACGTTGAGAGTGGC 240  
Db 181 CCGGCGGGGTTGACAGATGAGGGGAGGCTCGATTTCCGCGCGGACGTTGAGAGTGGC 240  
Qy 241 CAGCCTCGAAATCGCGAAACGCTGATTTTACCGGAGTTCGCCACAGATGATGGA 300  
Db 241 CAGCCTCGAAATCGCGAAACGCTGATTTTACCGGAGTTCGCCACAGATGATGGA 300  
Qy 301 CAAAGCCTGGGATAGTGGCCCTCGGATATTGACACTTGAAGGGCGGACCTACTGACAGAT 360  
Db 301 CAAAGCCTGGGATAGTGGCCCTCGGATATTGACACTTGAAGGGCGGACCTACTGACAGAT 360  
Qy 361 GAGGGCGGATCCTTGAACACTTGAAGGGGAGAGTGTGACAGATGAGGGGCGCACCTAT 420  
Db 361 GAGGGCGGATCCTTGAACACTTGAAGGGGAGAGTGTGACAGATGAGGGGCGCACCTAT 420  
Qy 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCCCGT 480  
Db 421 TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGAAGGGTTTCCGCCCGT 480  
Qy 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTCTCTTTTAAACCAATATTATATAAACCCTG 540  
Db 481 TTTTTCGGCCACCGCTAACCTGTCTTTTAACTCTCTTTTAAACCAATATTATATAAACCCTG 540  
Qy 541 TTTTAAACAGGGCTCGGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGCCTCCC 600  
Db 541 TTTTAAACAGGGCTCGGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGCCTCCC 600  
Qy 601 CTCTCGAACCTCCCGAAGATGTGCGGTGTAATACCGCACAGATGCGTAAGGAGA 660  
Db 601 CTCTCGAACCTCCCGAAGATGTGCGGTGTAATACCGCACAGATGCGTAAGGAGA 660  
Qy 661 AATACCGATCAGGCGCTCTCCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720  
Db 661 AATACCGATCAGGCGCTCTCCGCTTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720  
Qy 721 CGGCTCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCA 780  
Db 721 CGGCTCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCA 780  
Qy 781 GGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGAGAAAGGCGGAGGAAACCGTAAA 840  
Db 781 GGGGATAACGAGGAAAGAACATGTGAGCAAAAGGCGAGAAAGGCGGAGGAAACCGTAAA 840  
Qy 841 AAGGCGCGTGTGCGGCTTTTCCATAGGCTCGGCCCGCTCAGCAGATCACAAAAAT 900  
Db 841 AAGGCGCGTGTGCGGCTTTTCCATAGGCTCGGCCCGCTCAGCAGATCACAAAAAT 900  
Qy 901 CGACGCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAGATACCAAGGCTTTCC 960  
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Qy 961 CTTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCC 1020  
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Qy 1081 TCGGTGAGTTCGTTCCGCTCAAAGCTGGGTGTGTGACAGAAACCCCGCTTCAGCCCGAC 1140  
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Qy 1141 CGCTGGCCTTATCCGGTAACATATCGTCTTGAAGTCCAAACCGGTGTAAGACAGCTTATCG 1200  
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Qy 1321 AGCGCCATATTTAAAAGCTTACCAACGAAAGGATGAAGAGATGAGGAGGAGGAGATTG 1380  
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Qy 1381 CTTGTAATATATTGACAACTACTGATAAGATAATACTCTTTTATATAGAGATATCGCCG 1440  
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Qy 1501 GGGCAAGCATAAAACTTGCATGGAATAATGCTTGAACCCAGGACAAATAACCTTATAG 1560  
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Qy 1561 CTTGTAATTTTACCAAAATTTGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG 1620  
Db 1561 CTTGTAATTTTACCAAAATTTGTTTCAAAATCGGCTCCGTCGATACTATGTTATACG 1620  
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Qy 1681 GGAACAGTCAATGGAAGTTGCTGTTGATAATAGCTTCTTGGGCTGCTTTAAATACT 1740  
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Db 1741 GTAGAAAAGAGGAAAGAAATAATAATGCTTAAATGAGAATAATCACCGGAAATGAAAAA 1800  
Qy 1801 ACTGATCGAAAATAATACCGCTGCGTAAAAGATACGGAAGGAAATGCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAATAATACCGCTGCGTAAAAGATACGGAAGGAAATGCTCTGCTAAGGTATA 1860  
Qy 1861 TAAGCTGTTGGGAGAAATGAAAACCTATATTTAAAATGACGACAGCGGTATAAAG 1920  
Db 1861 TAAGCTGTTGGGAGAAATGAAAACCTATATTTAAAATGACGACAGCGGTATAAAG 1920  
Qy 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTTATGGCTGGAAGGAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTTATGGCTGGAAGGAAAGCTGCC 1980  
Qy 1981 TGTTCAAAAGGCTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA 2040  
Db 1981 TGTTCAAAAGGCTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATAGTGA 2040  
Qy 2041 GGGCGATGCGGCTCTTGTCTCGGAGAGTATGAAGTGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGGCGATGCGGCTCTTGTCTCGGAGAGTATGAAGTGAACAAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATGTCCTTA 2160  
Db 2101 CGAGCTGATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATGTCCTTA 2160  
Qy 2161 TACGAATAGCTTAGACAGCCGCTTAGCCGAATGGATTAATCTACTGTAATACGATCTGGC 2220  
Db 2161 TACGAATAGCTTAGACAGCCGCTTAGCCGAATGGATTAATCTACTGTAATACGATCTGGC 2220  
Qy 2221 CGATGTGATTCGGAAAACCTGGGAGAGACACTCCATTTAAAGATCCCGGCGAGCTGTA 2280  
Db 2221 CGATGTGATTCGGAAAACCTGGGAGAGACACTCCATTTAAAGATCCCGGCGAGCTGTA 2280

QY	2281	TGATTTTTAAAGACGAAAGCCCGAAGAGGAACCTGTCTTTTTCCACGGCGACCTGGG	2340
Db	2281		2340
QY	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341		2400
QY	2401	CGGAGGCGGACAAAGTGGTATGACATTCGCTCTCTGGCTCGGTTCGATCAGGAGGATAT	2460
Db	2401		2460
QY	2461	CGGGGAAGAACAGTATCTCGAGCTATTTTTTGACTTACTGGGATCAAGCTCGATTGGGA	2520
Db	2461		2520
QY	2521	GAAAAATAAAATATTATATTTTACTGGATGAATTGTTTTAGTACTAGATCTGGCGCAACG	2580
Db	2521		2580
QY	2581	ATCGCGGCGAACAGCAGGAGCGACCGACTCTTCGCGATCAAGTGTTCGCTCTCAGG	2640
Db	2581		2640
QY	2641	CCGAGGCCACGCGCAAGTATTTGGGCAAGGGTGCCTGGTATTTCGTGACGGCAAGATTC	2700
Db	2641		2700
QY	2701	GGATACCAAGTACGAGAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701		2760
QY	2761	AGGTGGATTATCTGGACACCAAGGCACAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761		2820
QY	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGAGGGTGAATGAATCGGACGCTTTGACCGGA	2880
Db	2821		2880
QY	2881	AGGCATACAGGCAAGAACTGATCGACGCGGGTTTTCCGCGGAGGATGCGCAAAACCATCG	2940
Db	2881		2940
QY	2941	CAAGCCGACCGTCAATCGCTGCGCCCGCGCAAACTTTCCAGTCCGCTCGGTTCGATGCTCC	3000
Db	2941		3000
QY	3001	AGCAAGCTACGGCCCAAGATCGAGCGGACACAGCGTGCAACTGGCTCCCGCTGCCCTGCGCG	3060
Db	3001		3060
QY	3061	CGCCATCGGCGCGCTGGAGCGTTTCGCTCTCGAAACAGGAGCGGCGAGGTTTGGCGA	3120
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QY	3121	AGTCGATGACATCGACACGCGAGGAACATGACGACCAAGAACGAAAAACCGCCGGCG	3180
Db	3121		3180
QY	3181	AGGACCTGGCAAAACAGTTCAGCGAGCGACAGCGGCGCGTTCGTAACACACAGCAAGC	3240
Db	3181		3240
QY	3241	AGCAGATCAAGGAATGCAGCTTTCTTGTTCGATATTGGCCGCTGGCGCGGACACGATGC	3300
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QY	3301	GAGCGATGCCAAACGACACGCGCCGCTCTGCGCTTGTTCACACCGCGCAACAGAAAAATCC	3360
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QY	3361	CGCGGAGGGCGCTGCAAAACAAAGTCTATTTTCCACGCTCAACAGGACGTGAAGATCACCT	3420

Db	3361	CGCGGAGGCGCTGCAAAACAAAGTCTATTTTCCACGCTCAACAGGACGTGAAGATCACCT	3420
QY	3421	ACACGGCGCTGAGCTGCGGGCGGACGATGAGAACTGCTGTGGCAGCAGGTGTTGGAGT	3480
Db	3421		3480
QY	3481	AGCGAAGCGCACCCCTATCTGGCGAGCCGATCACCTTACGTTCTACGAGCTTTGCGCAGG	3540
Db	3481		3540
QY	3541	ACCTGGCTGGTTCGATCAATGCGCGGTATTAACGAAAGCCGAGGAATGCTCTCGCGCC	3600
Db	3541		3600
QY	3601	TACAGCGAGCGGATGGGCTTACGTCGACCGCGTTGGGACCTGGATCGGTGCGC	3660
Db	3601		3660
QY	3661	TGCTGCACCGCTTCCGCGCTCTGGACCGTGGCAAGAAACGTCGCCGTTCGACGCTCTGA	3720
Db	3661		3720
QY	3721	TCGACGAGGAAATCGTCTGCTGTTTGTCTGGCGACCACTACAGAAATTCATATGGGAGA	3780
Db	3721		3780
QY	3781	AGTACCGCAAGCTGTCGCGACGGCCGAGGATGTCGACTATTTTACGCTCCGACCGGG	3840
Db	3781		3840
QY	3841	AGCGGTACCGCTCAAGCTTGGAAACCTTCGCGCTCATGTGCGGATCGEATTCACCCGCG	3900
Db	3841		3900
QY	3901	TGAAGAAGTGGCGAGCAGGTTCGCGAAGCCCTCGCGCTCATGTGCGGATCGGATTCACCCGCG	3960
Db	3901		3960
QY	3961	TGAAACACGCTGGGTCAATGATGACTGGTGATTCGAAACCTAGGCGCTTGTGGGGT	4020
Db	3961		4020
QY	4021	CAGTTCGCGCTGGGGTTTACGACCGCAGCGCTTTTACTGGCATTTCTTAGGTTGACGCTCTT	4080
Db	4021		4080
QY	4081	CTGATCGGCTGCTGTATCGAGTGGTGATTTTGTGCGGAGCTCCCGTTCGGGAGCTGTT	4140
Db	4081		4140
QY	4141	GGCTGGCTGGCGAGGATATTTGGTGTAAACAAATTCGACGCTTAGACAACTTAATA	4200
Db	4141		4200
QY	4201	ACACATTTGGGAGCTTTTAACTACTGGGGCTATCCCCGGGGGATATCATAGGCCCG	4260
Db	4201		4260
QY	4261	ATCTAGTAAACATAATGACACCGCGCGATAATTTATCTTAGTTTTCGCGCTATTTTTTG	4320
Db	4261		4320
QY	4321	TTTTCTATCCGCTATTAAATGATATAATGCGGACCTCTAATCAATAAAACCCATCTCATA	4380
Db	4321		4380
QY	4381	AATAAGCTCATGATTCATGTTAAATTTATTACATGCTTAAACGTAATTCACAGAAATAT	4440
Db	4381		4440
QY	4441	ATGATATATCATCGCAAGACCGGCAACAGGATTCATCTTTAAGAAACCTTTATTCGCAATG	4500
Db	4441		4500



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Db 4441 ATGATTAATCATCCAGACCGCAACAGGATTCAATCTTAAGAAACTTTATTGCCAAATG 4500
QY 4501 TTGGAACGATCGTTCGTGAGCTATGGCCCGGAGCTTGCCCGCGCTTAACACGCGTGG 4560
Db 4501 TTTGAACGATCGTTCGTGAGCTATGGCCCGGAGCTTGCCCGCGCTTAACACGCGTGG 4560
QY 4561 ATCTTTAATTAAGTCGACTCTAGAGAAATTCACCTC 4594
Db 4561 ATCTTTAATTAAGTCGACTCTAGAGAAATTAATTC 4594

RESULT 3
US-09-845-064-21
; Sequence 21, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10003
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pmrT1210
; NAME/KEY: rep origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColEI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
; OTHER INFORMATION: and P382, enabling the increase of the replication
; OTHER INFORMATION: rate
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976A1alaine synthetase terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4559)..(4572)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4594)..(5169)
; OTHER INFORMATION: Bar gene coding for phosphinothricine
; OTHER INFORMATION: acetyltransferase and glufosinate resistance
; FEATURE:
; NAME/KEY: intron
; LOCATION: (5170)..(5704)
; OTHER INFORMATION: Rice Actin Intron
; FEATURE:
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; NAME/KEY: promoter
; LOCATION: (5705)..(6638)
; OTHER INFORMATION: Rice Actin Promoter
; FEATURE:
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; LOCATION: (6646)..(6672)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6672)..(7107)
; OTHER INFORMATION: High Molecular Weight Glutenin promoter from wheat
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7107)..(7169)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: intron
; LOCATION: (7169)..(7687)
; OTHER INFORMATION: Rice Actin Intron
; FEATURE:
; NAME/KEY: gene
; LOCATION: (7688)..(9496)
; OTHER INFORMATION: GUS gene coding for beta glucuronidase
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (9497)..(9823)
; OTHER INFORMATION: No. US20030175976A1alaine synthetase terminator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9823)..(9996)
; OTHER INFORMATION: T-DNA right border
; US-09-845-064-21

Query Match 94.7%; Score 4549; DB 10; Length 10003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGCTGTTGCCCTCGCCCTGCGGCTGCGGCGCGGCGCGGCGGCGGCTGTGGATACCTGCGG 120
Db 1 CCGGGCTGTTGCCCTCGCCCTCGCCCTGCGGCTGCGGCGCGGCGGCTGTGGATACCTGCGG 60

QY 61 AAACGCGCTGGAAGCGCTGTGCGAGACACCGCGGCGCGGCGGCGGCGGCTGTGGATACCTGCGG 120
Db 61 AAACGCGCTGGAAGCGCTGTGCGAGACACCGCGGCGCGGCGGCGGCTGTGGATACCTGCGG 120

QY 121 AAAACTTGGCCCTCACTGACAGATGAGGGGCGGCGGCTGACACTTTCAGGGGCGGCGGCTCAC 180
Db 121 AAAACTTGGCCCTCACTGACAGATGAGGGGCGGCGGCTGACACTTTCAGGGGCGGCGGCTCAC 180

QY 181 CCGGCGCGCGCTTGACAGATGAGGGGCGGCGGCTCGATTTCGGCGGCGGCGGCTGAGAGTGGC 240
Db 181 CCGGCGCGCGCTTGACAGATGAGGGGCGGCGGCTCGATTTCGGCGGCGGCGGCTGAGAGTGGC 240

QY 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA 300
Db 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA 300

QY 301 CAAAGCTGGGGGATAAGTGCCTCGCGTATTGACACTTTCAGGGGCGGCGGCTTACTGACAGAT 360
Db 301 CAAAGCTGGGGGATAAGTGCCTCGCGTATTGACACTTTCAGGGGCGGCGGCTTACTGACAGAT 360

QY 361 GAGGGGCGCGATCCTTTGACACTTTCAGGGGCGGAGTGCTGACAGATGAGGGGCGGCGGCTAT 420
Db 361 GAGGGGCGCGATCCTTTGACACTTTCAGGGGCGGAGTGCTGACAGATGAGGGGCGGCGGCTAT 420

QY 421 TCACATTTGAGGGGCTGTCCACAGGCAAAAATCCAGCATTTTTCGAAGGGTTTCCGCGCGT 480
Db 421 TCACATTTGAGGGGCTGTCCACAGGCAAAAATCCAGCATTTTTCGAAGGGTTTCCGCGCGT 480

QY 481 TTTTCGGCCACCGCTAACTGCTTTTACCTGCTTTTAAACCAATATTTATAAACCTTG 540
Db 481 TTTTCGGCCACCGCTAACTGCTTTTAACTGCTTTTAAACCAATATTTATAAACCTTG 540
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QY	541	TTTTTAACAGGGCTGCGCCCTGTGCGGTGACCGCGACGCCGAAAGGGGGTGC	600
Db	541	TTTTTAACAGGGCTGCGCCCTGTGCGGTGACCGCGACGCCGAAAGGGGGTGC	600
QY	601	CTTCTCGAACCCTCCCGGAAGGTATGCGGTGTGAATAACCGCACAGATCGTAAGGAGA	660
Db	601	CTTCTCGAACCCTCCCGGAAGGTATGCGGTGTGAATAACCGCACAGATCGTAAGGAGA	660
QY	661	AAATACCGCATAGGGCGCTCTTCGGTCTCTCGCTACTGACTCGCTCGCTCGTTCGTT	720
Db	661	AAATACCGCATAGGGCGCTCTTCGGTCTCTCGCTACTGACTCGCTCGCTCGTTCGTT	720
QY	721	CGCTCGGGAGCGGTATCAGCTCACTCAAGCGGTATACGTTTATCCACAGAAATCA	780
Db	721	CGCTCGGGAGCGGTATCAGCTCACTCAAGCGGTATACGTTTATCCACAGAAATCA	780
QY	781	GGGGTAACACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAA	840
Db	781	GGGGTAACACGAGGAAGAACATGTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAA	840
QY	841	AAGCGCGCTTGTGCGGTTTTTCCATAGGCTCGCCCGCTGACGAGATCACAAAAT	900
Db	841	AAGCGCGCTTGTGCGGTTTTTCCATAGGCTCGCCCGCTGACGAGATCACAAAAT	900
QY	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTTCCC	960
Db	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGGCTTTCCC	960
QY	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGCCTCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCC	1020
QY	1021	GCCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCAAGCTGATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAGGTGGCGCTTCTCATAGCTCAAGCTGATCTCAGT	1080
QY	1081	TCGGTGTAGTCTGCTCCACAGCTGGCTGTGTCACGAAACCCCGCTTCAGCCGAC	1140
Db	1081	TCGGTGTAGTCTGCTCCACAGCTGGCTGTGTCACGAAACCCCGCTTCAGCCGAC	1140
QY	1141	CGCTGCGCTTATCCGGTAACATFCGTCTTGAGTCCAAACCGGTGAAGACAGCTTATCG	1200
Db	1141	CGCTGCGCTTATCCGGTAACATFCGTCTTGAGTCCAAACCGGTGAAGACAGCTTATCG	1200
QY	1201	CCTGCGCAGAGCTTCTACATAATCCGGATAAACCCAGCAACCTTTGAGGTGAT	1260
Db	1201	CCTGCGCAGAGCTTCTACATAATCCGGATAAACCCAGCAACCTTTGAGGTGAT	1260
QY	1261	AGGTAAGATTATACGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
Db	1261	AGGTAAGATTATACGAGGTATGAAACGAGAAATGGACCTTTACAGAAATTTACTCTATGA	1320
QY	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Db	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
QY	1381	CCTTGAATATATTGACAAATCTGTAAGATAAATACATCTTTTATATAGAGATATCGCG	1440
Db	1381	CCTTGAATATATTGACAAATCTGTAAGATAAATACATCTTTTATATAGAGATATCGCG	1440
QY	1441	TATGTAGGATTTTCCAGGGGCAAGGCATAGGACGCGCTTATCAATATATCTATAGAT	1500
Db	1441	TATGTAGGATTTTCCAGGGGCAAGGCATAGGACGCGCTTATCAATATATCTATAGAT	1500
QY	1501	GGGCAAGCATATAAACTTGCATGACTTAATGCTTTGAAACCCAGGACCAATAACCTTATAG	1560
Db	1501	GGGCAAGCATATAAACTTGCATGACTTAATGCTTTGAAACCCAGGACCAATAACCTTATAG	1560
QY	1561	CTTGTAATTTCTACAAAATTTGGTTTCAAAAATCGCGCTCGCTGATATGTTATACG	1620
Db	1561	CTTGTAATTTCTACAAAATTTGGTTTCAAAAATCGCGCTCGCTGATATGTTATACG	1620
QY	1621	CCAACTTTGAAACAACTTTGAAAAAGCTGTTTCTCGTATTTAAAGGTTTTTAGAATGCAA	1680

Db	1621	CCAACTTTGAAACAACTTTGAAAAAGCTGTTTCTCGTATTTAAAGTTTTTAGAATGCAA	1680
QY	1681	GGAAAGTGAATTTGGAGTTCTGTTATTAATAGCTTCTTGGGTATCTTTAAATACT	1740
Db	1681	GGAAAGTGAATTTGGAGTTCTGTTATTAATAGCTTCTTGGGTATCTTTAAATACT	1740
QY	1741	GTAGAAAAAGAGGAAGAAATAATTAATGCTAAAAATGAGAAATATCACCGAAATGAAAAA	1800
Db	1741	GTAGAAAAAGAGGAAGAAATAATTAATGCTAAAAATGAGAAATATCACCGAAATGAAAAA	1800
QY	1801	ACTGATCGAAAAATACCGTTCGCTAAAAATACGGAAGGAATGTCTCTGCTTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGTTCGCTAAAAATACGGAAGGAATGTCTCTGCTTAAGGTATA	1860
QY	1861	TAAGCTGGTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTATTAAGG	1920
Db	1861	TAAGCTGGTGGGAGAAATGAAAACTTATTTAAAAATGACGACAGCGGTATTAAGG	1920
QY	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTATGGCTGGAAGGAAGCTGCC	1980
QY	1981	TGTTCCAAAAGTCTCTGACCTTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTCCAAAAGTCTCTGACCTTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
QY	2041	GGCGGATGGCTCTTTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCGGATGGCTCTTTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
QY	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACCTCCATCGACATATCGGATTTGCCCTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCATCAGGCTCTTTCACCTCCATCGACATATCGGATTTGCCCTA	2160
QY	2161	TACGAATAGCTTACAGACGCGCTTACCGAAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTACAGACGCGCTTACCGAAATTTGGATTTACTTACTGAATAACGATCTGGC	2220
QY	2221	CGATGTGGATTTGCGAAACCTGGGAAAGACACTCCATTTAAAGATCCGCGGAGCTGTA	2280
Db	2221	CGATGTGGATTTGCGAAACCTGGGAAAGACACTCCATTTAAAGATCCGCGGAGCTGTA	2280
QY	2281	TGATTTTTTAAAGACGGAAGGCCGAAAGGAATTTGCTTTCCACACGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACGGAAGGCCGGAAGGAATTTGCTTTCCACACGCGACCTGGG	2340
QY	2341	AGACAGCAACATCTTTGTGAAAGATGCGCAAAAGTAAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGCGCAAAAGTAAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
QY	2401	CGGCGGCGGACAAGTGTATGACATTTGCCTTCGCTCCGCTCGATCAGGGAGGATAT	2460
Db	2401	CGGCGGCGGACAAGTGTATGACATTTGCCTTCGCTCCGCTCGATCAGGGAGGATAT	2460
QY	2461	CGGGAAGAACAGTATGTCTGAGCTATTTTGTACTTACTCGGGATCAAGCTCGATTGGGA	2520
Db	2461	CGGGAAGAACAGTATGTCTGAGCTATTTTGTACTTACTCGGGATCAAGCTCGATTGGGA	2520
QY	2521	GAAAAATAAATATTTATTTTACTGGAATGAATTTTGTAGTACTAGATGTGGCGCAACG	2580
Db	2521	GAAAAATAAATATTTATTTTACTGGAATGAATTTTGTAGTACTAGATGTGGCGCAACG	2580
QY	2581	ATGCGCGGCAACAGCAGGAGCGCACCGACTCTTTCGCGATCAAGTGTTCCTCAGG	2640
Db	2581	ATGCGCGGCAACAGCAGGAGCGCACCGACTCTTTCGCGATCAAGTGTTCCTCAGG	2640
QY	2641	CCGAGGCCCAACAGTATTTTGGCAAGGGGTCTGCTGTTTTCGTCAGGCGCAAGATTC	2700
Db	2641	CCGAGGCCCAACAGTATTTTGGCAAGGGGTCTGCTGTTTTCGTCAGGCGCAAGATTC	2700
QY	2701	GGAAATACAAAGTACGAGAAAGGACGGGCGACGCTCTACGGAACCGACTTCATTCGCCGATA	2760

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Db 2701 GGAATACCAAGTACGAGAAAGGACGGCCAGACGGTCTACGGGACCGACTTCATTTCGCCGATA 2760
Qy 2761 AGGTGGATTATCTGGACACCAAGGACACAGGCGGGTCAAAATCAGGAATAAGGGCACATTG 2820
Db 2761 AGGTGGATTATCTGGACACCAAGGACACAGGCGGGTCAAAATCAGGAATAAGGGCACATTG 2820
Qy 2821 CCCCAGGCTGAGTTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGACGTTTGAACCGGA 2880
Db 2821 CCCCAGGCTGAGTTCGGGGCAATCCCGCAAGGAGGTTGAATGAATCGACGTTTGAACCGGA 2880
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Qy 2941 CAAGCCGACCGTCATCGCTGCGGCCCGCGAAACCTTCCAGTCCGTCGGCTCGATGGTCC 3000
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Db 3121 AGTCGATGACCATCGACACGCGAGGAATATGACGACCAAGAACGCAAAACCGCCGCG 3180
Qy 3181 AGGACCTGGCAAAACAGGTTCAGCGAGGCCAAGCAGCGCGTTCGTAACACACGAAAGC 3240
Db 3181 AGGACCTGGCAAAACAGGTTCAGCGAGGCCAAGCAGCGCGTTCGTAACACACGAAAGC 3240
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Db 3421 ACACCGCGCTCGAGCTCGGGCCGACGATGACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480
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Db 3781 AGTACCGCAAGCTGTCCCGACCGGCCGACGGAATGTCGACTATTTTCAGCTCGCACCGG 3840
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Db 3841 AGCCGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTCCGATCGGATTCACCCGCG 3900
Qy 3901 TGAAGAAGTGGCCGAGCAGCTCGGGAAGCCTTCCGAGAGTTCGCGAGGACGCGGCTGG 3960
Db 3901 TGAAGAAGTGGCCGAGCAGCTCGGGAAGCCTTCCGAGAGTTCGCGAGGACGCGGCTGG 3960
Qy 3961 TGAACAACGCGCTGGGTCAATGATGACCTGGTGCAATTCGAAACGCTAGGGCTTGTGGGT 4020
Db 3961 TGAACAACGCGCTGGGTCAATGATGACCTGGTGCAATTCGAAACGCTAGGGCTTGTGGGT 4020
Qy 4021 CAGTTCGGCTGGGGTTTACGACGCGCCTTACTGGCAATTCCTAGAGTTGACGCTTT 4080
Db 4021 CAGTTCGGCTGGGGTTTACGACGCGCCTTACTGGCAATTCCTAGAGTTGACGCTTT 4080
Qy 4081 CTGATGGGCTGCCCTGTATCGAGTGGTGATTTTGTGCGGAGCTGCCGTCCGGGAGCTGTT 4140
Db 4081 CTGATGGGCTGCCCTGTATCGAGTGGTGATTTTGTGCGGAGCTGCCGTCCGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGCAGGATATATTGGTGTAAACAAATTCAGCGCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGCAGGATATATTGGTGTAAACAAATTCAGCGCTTAGACAACTTAATA 4200
Qy 4201 ACACATTGGCGACGTTTTTAATGTAATGCTGGGGCTATCCCCGGGGGATATCCATAGGCCG 4260
Db 4201 ACACATTGGCGACGTTTTTAATGTAATGTAATGCTGGGGCTATCCCCGGGGGATATCCATAGGCCG 4260
Qy 4261 ATCTAGTAACATAATGACACCGCGCGGATAAATTTATCTAGTTTGGCGCTATATTTTG 4320
Db 4261 ATCTAGTAACATAATGACACCGCGCGGATAAATTTATCTAGTTTGGCGCTATATTTTG 4320
Qy 4321 TTTTCTATCGCGTATTAATGTAATGTAATGCGGACCTATATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCGCGTATTAATGTAATGTAATGCGGACCTATATATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTCATGCAATTACATGTTTAAATTTATACATGCTTAACTGTAATCAACAGAAATAT 4440
Db 4381 AATAACGTCATGCAATTACATGTTTAAATTTATACATGCTTAACTGTAATCAACAGAAATAT 4440
Qy 4441 ATGATTAATCATCCCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Db 4441 ATGATTAATCATCCCAAGACCGGCAACAGGATTCATCTTAAGAACTTTATTCGCAATG 4500
Qy 4501 TTTTGAACGATCGTTCGCGAGCTATCGGCCGAGCTTGGCCGCGGTT 4549
Db 4501 TTTTGAACGATCGTTCGCGAGCTATCGGCCGAGCTTGGCCGCGGTT 4549
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## RESULT 4

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US-09-845-064-16
; Sequence 16, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 5614
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; pmr1202
; FEATURE:
; NAME/KEY: rep_origin
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; LOCATION: (1)...(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColEI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycinin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: trfA locus from RK2 coding for two proteins, P285
; OTHER INFORMATION: and p382, enabling the increase of the rate of
; OTHER INFORMATION: replication
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4575)..(5150)
; OTHER INFORMATION: Bar gene coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase and herbicide resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5150)..(5368)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5368)..(5434)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5434)..(5607)
; OTHER INFORMATION: T-DNA right border
;
US-09-845-064-16

Query Match      94.3%; Score 4531.4; DB 10; Length 5614;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCTATGGCCCTGCAAAACGGCCAG 60
Db      1  CCGGGCTGGTTGCCCTCGCCGCTGGGCTGGCGCGCTATGGCCCTGCAAAACGGCCAG 60

Qy     61  AAACCGCGTGAAGCCGTTGTCGAGACACACCGCGCGCGCGCGGTTGTGGATACCTCGCGG 120
Db     61  AAACCGCGTGAAGCCGTTGTCGAGACACACCGCGCGCGCGCGGTTGTGGATACCTCGCGG 120

Qy    121  AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180
Db    121  AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180

Qy    181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGAGCTGGAGCTGGC 240
Db    181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGCGAGCTGGAGCTGGC 240

Qy    241  CAGCCTCGCAATCGGCGAAACGCTGATTTACGCGAGTTTCCACAGATGATGTGA 300
Db    241  CAGCCTCGCAATCGGCGAAACGCTGATTTACGCGAGTTTCCACAGATGATGTGA 300

Qy    301  CAACGCTGGGATTAAGTCCCTCGCGTATTGACACTTGAGGGGCCGACTACTGACAGAT 360
Db    301  CAACGCTGGGATTAAGTCCCTCGCGTATTGACACTTGAGGGGCCGACTACTGACAGAT 360

Qy    361  GAGGGCGCGATCCTTGACACTTGAGGGCGAGAGTGCTGACAGATGAGGGCGCACCTAT 420

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Db 1441 TATGTAAGGATTTTCAGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAT 1500  
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Db 1501 GGGCAAAAGCATAAAACTTGCATGCACTAATGCTTGAAACCCAGGACAATAACCTTATAG 1560  
Qy 1561 CTTGTAAATTTCTACCAAAATTTGGTTTTCAAAATTCGGCTCCGTCGATACCTATGTTATACG 1620  
Db 1561 CTTGTAAATTTCTACCAAAATTTGGTTTTCAAAATTCGGCTCCGTCGATACCTATGTTATACG 1620  
Qy 1621 CCAACTTTGAAACCAACTTTGAAAGAGCTGTTTCTGGTATTTAAAGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAACCAACTTTGAAAGAGCTGTTTCTGGTATTTAAAGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGGAGTTCTGTTTATAAATTTAGCTTCTTGGGGTATCTTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTCTGTTTATAAATTTAGCTTCTTGGGGTATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTTAAATGAGAAATATCACCGGAAATGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTTAAATGAGAAATATCACCGGAAATGAAAAA 1800  
Qy 1801 ACTGATCGAAATAATACCGCTCGCTTAAAGATACGGAAGGAATGCTCTCTCTAAGGTATA 1860  
Db 1801 ACTGATCGAAATAATACCGCTCGCTTAAAGATACGGAAGGAATGCTCTCTCTAAGGTATA 1860  
Qy 1861 TAAAGCTGGTGGGAGAAAATGAAAACCTTATATTTAAATAACACGACAGCCGGTATAAAGG 1920  
Db 1861 TAAAGCTGGTGGGAGAAAATGAAAACCTTATATTTAAATAACACGACAGCCGGTATAAAGG 1920  
Qy 1921 GACCACCTATGATGTGGAAACCGGAAAAGGACATGATGCTATGCTGGAAGAAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGGAAACCGGAAAAGGACATGATGCTATGCTGGAAGAAAAGCTGCC 1980  
Qy 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACCGGCATGATGCTGGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCGAAAGGCTCTGCACCTTTGAAACCGGCATGATGCTGGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCAGATGGCGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCAGATGGCGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATCGGAGTGCAATCAGGCTCTTTTCACTCCATCGACATATCGGAATGTCCTTA 2160  
Db 2101 CGAGCTGTATCGGAGTGCAATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Qy 2161 TACGAATAGCTTAGACAGCCGCTTAGCCGAATTTGGATTGGAATTAATTAACGATCTGCC 2220  
Db 2161 TACGAATAGCTTAGACAGCCGCTTAGCCGAATTTGGATTGGAATTAATTAACGATCTGCC 2220  
Qy 2221 CGATGTGGATTGCGAAAACCTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA 2280  
Db 2221 CGATGTGGATTGCGAAAACCTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA 2280  
Qy 2281 TGAATTTTAAAGACCGAAAGCCCGAAGAGAACTTTGCTTTTCCACGCGCACTGGG 2340  
Db 2281 TGAATTTTAAAGACCGAAAGCCCGAAGAGAACTTTGCTTTTCCACGCGCACTGGG 2340  
Qy 2341 AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTAATCTTGGGAGAAG 2400  
Db 2341 AGACAGCAACATCTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTAATCTTGGGAGAAG 2400  
Qy 2401 CGGCGGGCGGACAAGTGGTATGACATTCGCTTCTGGCTCCGTCGATCAGGGAGGATAT 2460  
Db 2401 CGGCGGGCGGACAAGTGGTATGACATTCGCTTCTGGCTCCGTCGATCAGGGAGGATAT 2460  
Qy 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTTGGGATCAAGCCCTGATTGGGA 2520  
Db 2461 CGGGGAAGAACAGTATGTCGAGCTATTTTGTGACTTACTTGGGATCAAGCCCTGATTGGGA 2520  
Qy 2521 GAAAAATAAATATTTATTTTACTGATGAATTTGTTTTAGTACCTAGATGTGGCGCAACG 2580  
Db 2521 GAAAAATAAATATTTATTTTACTGATGAATTTGTTTTAGTACCTAGATGTGGCGCAACG 2580

Qy 2581 ATCCCGCGCAAAAGCAGGAGCGCACCGACTTCTTTCCGCAATCAAGTGTGTTTGGCTCTCAGG 2640  
Db 2581 ATCCCGCGCAAAAGCAGGAGCGCACCGACTTCTTTCCGCAATCAAGTGTGTTTGGCTCTCAGG 2640  
Qy 2641 CCAGAGCCCAACGGCAAGTATTTGGGCAAGGGTTCGCTGTTATTCGTGACAGGCAAGATTC 2700  
Db 2641 CCAGAGCCCAACGGCAAGTATTTGGGCAAGGGTTCGCTGTTATTCGTGACAGGCAAGATTC 2700  
Qy 2701 GGAATACCAAGTACGAGAGGAGCGGCAGACGCTCTACGGGACCGACTTCTCATTTGCCGATA 2760  
Db 2701 GGAATACCAAGTACGAGAGGAGCGGCAGACGCTCTACGGGACCGACTTCTCATTTGCCGATA 2760  
Qy 2761 AGTGTGATTATCTTGGACACCAAGGCACACGAGCGGGTCAATATCAGGAATTAAGGACATTCG 2820  
Db 2761 AGTGTGATTATCTTGGACACCAAGGCACACGAGCGGGTCAATATCAGGAATTAAGGACATTCG 2820  
Qy 2821 CCCCGCGGTGAGTTCGGGGCAATCCCGAAGGAGGGTGAATGAATCGGAACGTTTTGACCGGA 2880  
Db 2821 CCCCGCGGTGAGTTCGGGGCAATCCCGAAGGAGGGTGAATGAATCGGAACGTTTTGACCGGA 2880  
Qy 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGTTCGCGCGAGGATGCCGAAACCATCG 2940  
Db 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGTTCGCGCGAGGATGCCGAAACCATCG 2940  
Qy 2941 CAAAGCCGACCGTATGCGGTGCGCCCGGAAAACCTTCCAGTCCGTCCGTCGATGGTCC 3000  
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Qy 3001 AGCAAGCTACGCGCAAGAGTTCGAGCGGCAAGCGTGCCTGCTCGAAACAGGAGCGGAGTTGGCGA 3120  
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Qy 3121 AGTCGATGACCAATCGACACGCGAGGAATATGACGACCAAGAACGAAACCCGCGGCG 3180  
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Qy 3181 AGGACCTGGCAAAACAGGTCAGCGAGGCAAGCAGCGCCGCTTGTGTAACACACGAAAGC 3240  
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Qy 3721 TCACGAGGAAATCGTCTGCTGCTGTTCTGCTGGCCACCACTACAGAAATTCATATGGGAGA 3780
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Qy 3781 AGTACCGCAAGCTGTGCCCGACCGCCGACGAGTGTTCGACTATTTTCAGCTCCGACCGGG 3840
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Qy 3901 TGAAGAAGTGGCGGACGAGTGGCGAAGCCTGCGAAGAGTTGCGAGGACGGCGCTGG 3960
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Db 4501 TTTGAACGATCGTTTCGTCGAGCTATGGGCCCTA 4533
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; Sequence 3, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: Synvec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27

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; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 5971  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pmrI118  
; FEATURE:  
; NAME/KEY: rep_origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep_origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus from pRK2 coding for two proteins,  
; OTHER INFORMATION: P285 and P382, enabling the increase in the rate  
; OTHER INFORMATION: of replication  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976A1alaline synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4560)..(5556)  
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase  
; OTHER INFORMATION: and kanamycin resistance  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (5557)..(5770)  
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; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5791)..(5964)  
; OTHER INFORMATION: T-DNA right border  
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; NAME/KEY: misc feature  
; LOCATION: (5770)..(5791)  
; OTHER INFORMATION: MCS multiple cloning site  
US-09-845-064-3
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Query Match 94.3%; Score 4531.4; DB 10; Length 5971;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCGCGCTCTATGGCCCTGCAACGCGCCAG 60  
Db 1 CCGGGCTGGTTGCCCTCGCGCTGGGCTGGCGCGCGCTCTATGGCCCTGCAACGCGCCAG 60  
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Db 61 AAACGCGCTCGAAGCCGTTGTGCAGACACCGCGCGCGCGCGGCTGTGGATACCTCCGG 120  
Qy 121 AAACCTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCCGACTCAC 180  
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Qy 181 CCGGCGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTCCGGCGCGGACGTTGGAGCTGGC 240  
Db 181 CCGGCGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTCCGGCGCGGACGTTGGAGCTGGC 240
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Db 181 CCGCGCGCGGTTGACAGATGAGGGCAGGCTCGATTTCCGCGCGCGACCTGGAGCTGGC 240  
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Db 241 CAGCCTCGCAATCGCGGAAAGCCCTGATTTTACGCGAGTTCCTCCACAGATGATGGGA 300  
Qy 301 CAAGCCTGGGGATAAGTGCCTCGGGTATTGACACTTTGAGGGGCGGACTACTGACAGAT 360  
Db 301 CAAGCCTGGGGATAAGTGCCTCGGGTATTGACACTTTGAGGGGCGGACTACTGACAGAT 360  
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Db 361 GAGGGGCGCATCCTTGACACTTTGAGGGCAGAGTCTGACAGATGAGGGGCGCACCTAT 420  
Qy 421 TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCAATTCGAAGGGTTCCGCGCGT 480  
Db 421 TGACATTTGAGGGGCTGTCCACAGGCAGAAATCCAGCAATTCGAGGGTTCCGCGCGT 480  
Qy 481 TTTTCGGCCACCGGTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540  
Db 481 TTTTCGGCCACCGGTAACTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540  
Qy 541 TTTTAAACAGGGCTGCGCCCTGCGCGTGACCGCGCAGCGGAGGGGGTGCCCCC 600  
Db 541 TTTTAAACAGGGCTGCGCCCTGCGCGTGACCGCGCAGCGGAGGGGGTGCCCCC 600  
Qy 601 CTTTCTCGAACCCCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGGTAAGAGA 660  
Db 601 CTTTCTCGAACCCCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATCGGTAAGAGA 660  
Qy 661 AAATAACGCATCAGGGGCTCTTCGGTCTCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720  
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Qy 721 CGGCTGCGGCGAGGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGATCA 780  
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Db 781 GGGGTAATACCGAGAAAGAACTGTGAGCAAAAGGCGAGCAAGGCGCAGAACCGTAA 840  
Qy 841 AAGGCGCGTGTGCGGTTTTTCCATAGGCTCCGCCCCCTTCAAGAGCATCAAAAAAT 900  
Db 841 AAGGCGCGTGTGCGGTTTTTCCATAGGCTCCGCCCCCTTCAAGAGCATCAAAAAAT 900  
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Db 901 CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACAGGGCTTCCC 960  
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Db 961 CTTGGAAGCTCCCTCGTGGGCTCTCTGTTCCGACCTGCGGCTTACCGGATACCTGTCC 1020  
Qy 1021 GCCTTTCTCCCTTCGGGAAGCGTGGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080  
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Db 1201 CCACTGGCAGCAGCTTCTACCAATATCCGCGATAAACCCAGCGAACCAATTTGAGGTGAT 1260  
Qy 1261 AGGTAAGATPATACGAGGTATGAAACCGAGAAATCGACTTTACAGAAATTAATCTATGA 1320  
Db 1261 AGGTAAGATPATACGAGGTATGAAACCGAGAAATCGACTTTACAGAAATTAATCTATGA 1320

Qy 1321 AGCGCCATATTTAAAAAGCTTACCAAGACGAAGAGGATGAAGAGGATGAGGAGCAGATTG 1380  
Db 1321 AGCGCCATATTTAAAAAGCTTACCAAGACGAAGAGGATGAAGAGGATGAGGAGCAGATTG 1380  
Qy 1381 CTTTGAATATATTGACAACTACTGATAAAGATAATACATCTTTTATATAGAAAGATATCGCCG 1440  
Db 1381 CTTTGAATATATTGACAACTACTGATAAAGATAATACATCTTTTATATAGAAAGATATCGCCG 1440  
Qy 1441 TATGTAAGGATTTTACGGGGCAAGGCATAGGACGCGCTTATCAATATATATCTATAGAAT 1500  
Db 1441 TATGTAAGGATTTTACGGGGCAAGGCATAGGACGCGCTTATCAATATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAAACTTTGCATGGACTAATGCTTGAAGCCCAAGGACAAATAACCTTATAG 1560  
Db 1501 GGGCAAGCATAAAACTTTGCATGGACTAATGCTTGAAGCCCAAGGACAAATAACCTTATAG 1560  
Qy 1561 CTTTGAATTTTACCAAAATTTGGTTTCAAAATCGGCTCGATCTATGTATTATAG 1620  
Db 1561 CTTTGAATTTTACCAAAATTTGGTTTCAAAATCGGCTCGATCTATGTATTATAG 1620  
Qy 1621 CCAACTTTGAAACCAACTTTGAAAAAGCTGTTTTCTGGTATTTAAGTTTTAGAAATGCAA 1680  
Db 1621 CCAACTTTGAAACCAACTTTGAAAAAGCTGTTTTCTGGTATTTAAGTTTTAGAAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGAGAGTTTCGTCCTTGTATATAATTTAGCTTCTTTGGGCTATCTTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGAGAGTTTCGTCCTTGTATATAATTTAGCTTCTTTGGGCTATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAAGAGGAAGAAATAATAATGCTTAAATGAGAAATATACCGGAAATGAAAAA 1800  
Db 1741 GTAGAAAAAGAGGAAGAAATAATAATGCTTAAATGAGAAATATACCGGAAATGAAAAA 1800  
Qy 1801 ACTGATCGAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
Qy 1861 TAACTGCTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGAGCAGCGGTATAAAGG 1920  
Db 1861 TAACTGCTGGGAGAAAAATGAAAAACCTATATTTAAAAATGACGAGCAGCGGTATAAAGG 1920  
Qy 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
Qy 1981 TGTTCGAAAGGCTCTGCACTTTGAAACGGGATGATGCTGGAAGGAAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCGAAAGGCTCTGCACTTTGAAACGGGATGATGCTGGAAGGAAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCAGATGCGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Db 2041 GGCAGATGCGCTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Db 2101 CGAGCTGTATGCGGAGTGCATCAGGCTCTTTTCACTCCATCGACATATCGGATTTGCCCTA 2160  
Qy 2161 TAGGAATAGCTTTAGACAGCGGCTTAGCCGAAATGGATTTACTTACTCAATAACCATCTGCC 2220  
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Qy 2221 CGATGTGGATTCGAAAACTCGGAAGAGACACTCCATTTTAAAGATCCCGCGAGCTGTA 2280  
Db 2221 CGATGTGGATTCGGAAGAACTCGGAAGAGACACTCCATTTTAAAGATCCCGCGAGCTGTA 2280  
Qy 2281 TGATTTTTTAAAGACGGAAGCCCGGAGGAACTTGTCTTTTCCACCGGCACTGGG 2340  
Db 2281 TGATTTTTTAAAGACGGAAGCCCGGAGGAACTTGTCTTTTCCACCGGCACTGGG 2340  
Qy 2341 AGACAGCAACATCTTTTGTGAAAAGATGGCAAGTAAAGTGGCTTTTATGTATCTTGGGAGAG 2400  
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Qy	2401	CGGCAGGCGCGCAAGTGGTATGACATTGGCTTCTCGGTCCGGTCCGATCAGGAGGATAT	2460
Db	2401		2460
Qy	2461	CGGCAGGCGCGCAAGTGGTATGACATTGGCTTCTCGGTCCGATCAGGAGGATAT	2460
Db	2461		2460
Qy	2461	CGGGGAAGAACAGTATGTCAGAGCTATTTTTGACTTACTCGGGATCAAGCCTGATTGGGA	2520
Db	2461		2520
Qy	2521	GAATAAATAATATATATTTTCTGGATGAATTTGTTTATGATCCTAGATGTCGGCGCAAG	2580
Db	2521		2580
Qy	2581	ATGCGCGGCAAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581		2640
Qy	2641	CCGAGGCCCAAGTATTTTGGGCAAGGGTCCGCTGGTATTCGTCAGGCGCAAGATTC	2700
Db	2641		2700
Qy	2701	GGAAATCAAGTACGGAAGGACGGCCAGACGGTCTACGGGACCGACTTCAATTCGCGGAT	2760
Db	2701		2760
Qy	2761	AGGTGGATTATCTGGACACCAAGGCACAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761		2820
Qy	2821	CCCCGGCGTAGTCGGGCGCAATCCCGCAAGGAGGGTGAATGAATTCGGACGCTTTGACCGGA	2880
Db	2821		2880
Qy	2881	AGGCATACAGCAAGAACTATGATCGACCGGGGTTTTCCGCGAGGATCGCGAAACCATCG	2940
Db	2881		2940
Qy	2941	CNAGCCGACGTCATCGGTGCGCCCGCGAAACCTTCCAGTCGCTCGGCTCGATGTC	3000
Db	2941		3000
Qy	3001	AGCAAGCTAGCGGCAAGATCGAGCGCGACAGCGTGCACCTGGCTCCGCCCTGCCCTGCCCG	3060
Db	3001		3060
Qy	3061	CGCCATCGGCGCGGTGGAGCGTTTCGGTCTCTCGAACAGGAGCGCGAGTTTGGCGA	3120
Db	3061		3120
Qy	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGCCAGCAAGCGGAAACCGCGCGCG	3180
Db	3121		3180
Qy	3181	AGGACCTGGCAAAACAGGTCAAGCAGGCGCAAGCAGCGCGCTTCTGTAACACACGAAAGC	3240
Db	3181		3240
Qy	3241	AGCAGATCAAGAAATGACGCTTTCCTTTGTCGATATTTGCGCCGTGGCGGACACGATGC	3300
Db	3241		3300
Qy	3301	GAGCGATGCCAAACGACACGCGCGCTCTGCCCTGTTTCCACCAGCGCAACAGAAATCC	3360
Db	3301		3360
Qy	3361	CGCGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCAACAAAGGACGTTGAAGATCACCT	3420
Db	3361		3420
Qy	3421	ACACCGGCTCGAGCTCGCGGCGGACGATGCGAACTGGTGTGGCAGGAGTGTGGAGT	3480
Db	3421		3480
Qy	3481	ACGGAAGCGCACCCCTATCGGCGAGCGGATCACCTTTCACGTTCTACGAGCTTTGGCAGG	3540
Db	3481		3540

RESULT 6

Db	3481	ACGGAAGCGCACCCCTATCGGCGAGCCGATCACCTTTCAGGCTTTCAGGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGGTTCGATCAATAGCCGGTATTAACAGAAAGCCGAGGAATGCTGTTCGGCC	3600
Db	3541		3600
Qy	3601	TACAGCGGACGGGATGGGCTTTCACGTCGACCGCGTTCGGCACCTTGGGAATCGGTGTCG	3660
Db	3601		3660
Qy	3661	TGCTGCACCGCTTCCCGCTCCTGGACCGTGGCAAGAAACGTCCTCCGTTTGCAGGCTCTGA	3720
Db	3661		3720
Qy	3721	TCGACGAGGAAATCGTCTGCTGTTTGTCTGGGACCACTACACGAAATTCATATGGGAGA	3780
Db	3721		3780
Qy	3781	AGTACCGCAAGCTGTCGCGGACGGCCGACGGATGTTTCGACTATTTTTCAGCTCGACCGGG	3840
Db	3781		3840
Qy	3841	AGCGGTACCCGCTCAAGCTGGAAACCTTCCGCTCATGTGCGGATCGGATTCACCCGCG	3900
Db	3841		3900
Qy	3901	TGAAGAGTGGCGGACGAGGTTCGGGAGCGCTTGCAGAAAGTTTGCAGGAGCGGCTGG	3960
Db	3901		3960
Qy	3961	TGAAACACCCCTGGGCTCAATGATGACCTGGTGCATTTGCAACCGTAGGGCTTTGGGGT	4020
Db	3961		4020
Qy	4021	CAGTTCGGCTGGGGTTTCAGCAGCAGCGCTTTTACTTGGCATTTCTAGGTTCAGCTCTT	4080
Db	4021		4080
Qy	4081	CTGATGGGCTGCTGTATCAGTGGTGTATTTTGTGCGGAGCTCCCGTTCGGGAGCTGTT	4140
Db	4081		4140
Qy	4141	GGCTGGCTGGGACGATATATTTGGTGTAAACAAATTCAGCTTTAGACAACTTAATA	4200
Db	4141		4200
Qy	4201	ACACATTCGGGACGTTTTTAACTGCTGGGCTATCCCCGGGGGATATCCATAGGCGCG	4260
Db	4201		4260
Qy	4261	ATCTAGTAACATTAATGACACCGCGCGGATATTTTATCTCTAGTTTGGCGCTATATTTG	4320
Db	4261		4320
Qy	4321	TTTTCTATCGGCTTAAATGATATATTCGGGACTCTAATCATATAAAACCCATCTCAT	4380
Db	4321		4380
Qy	4381	AATAAGCTCATGCAATACATGTTTAAATTTATACATGCTTAAACGTAATTCACAGAAATAT	4440
Db	4381		4440
Qy	4441	ATGATAATCATTCGCAAGACCGGCAACAGGATTCATCTTAAAGAACTTTATTCGCAATG	4500
Db	4441		4500
Qy	4501	TTTGAACGATCGTTTCGTCGAGCTATGGGCCGA 4533	
Db	4501		
Qy	4501	TTTGAACGATCGTTTCGTCGAGCTATGGGCCAA 4533	
Db	4501		

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US-09-845-064-4
; Sequence 4, Application US/09845064
; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 4
; LENGTH: 6016
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pMRT1119
; FEATURE:
; NAME/KEY: rep origin
; LOCATION: (1)-(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori ColEI
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus coding for two proteins, p285 and p382,
; OTHER INFORMATION: enabling the increase in the rate of replication
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Ala1ine synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4560)..(5556)
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase
; OTHER INFORMATION: and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5770)
; OTHER INFORMATION: No. US20030175976Ala1ine synthetase promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5835)..(6009)
; OTHER INFORMATION: T-DNA right border
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5770)..(5836)
; OTHER INFORMATION: MCS multiple cloning site
; US-09-845-064-4

Query Match      94.3%; Score 4531.4; DB 10; Length 6016;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CCGGGCTGGTTCCTCGCGCTGGGCTGGGCGCGCTATGGCCCTGCAAAACGCCCCAG 60
Db      1  CCGGGCTGGTTCCTCGCGCTGGGCTGGGCGCGCTATGGCCCTGCAAAACGCCCCAG 60

61  AAACGCCGTCGAAGCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCGG 120
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61  AAACGCCGTCGAAGCGTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCGG 120

121  AAAAATTGGCCCTCACTGACAGATGAGGGCGGACCTTGACACTTGAGGGCGGCACTCAC 180
    |||||
121  AAAAATTGGCCCTCACTGACAGATGAGGGCGGACCTTGACACTTGAGGGCGGCACTCAC 180

181  CCGCGCGCGCTTGTACAGATGAGGGCGGACCTCGATTTTCGGCGCGGCGACCTGGAGCTGGC 240
    |||||
181  CCGCGCGCGCTTGTACAGATGAGGGCGGACCTCGATTTTCGGCGCGGCGACCTGGAGCTGGC 240

241  CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300
    |||||
241  CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGGAGTTTCCACAGATGATGGA 300

301  CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGCGGCGACTACTGACAGAT 360
    |||||
301  CAAGCCTGGGGATAAGTGCCTCGGTATTGACACTTGAGGGCGGCGACTACTGACAGAT 360

361  GAGGGCGCGGATCCTTTGACACTTTGAGGGCGGAGAGTGTCTGACAGATGAGGGCGGCGACCTAT 420
    |||||
361  GAGGGCGCGGATCCTTTGACACTTTGAGGGCGGAGAGTGTCTGACAGATGAGGGCGGCGACCTAT 420

421  TGACATTTGAGGGCTGTTCACAGGAGAAATCCAGCATTTTCAAGGGTTTCGGCCCGT 480
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421  TGACATTTGAGGGCTGTTCACAGGAGAAATCCAGCATTTTCAAGGGTTTCGGCCCGT 480

481  TTTTCGGCCACCGCTAACCTGTCTTTAACTGCTTTTAAACCAATATTTATAACCTTG 540
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481  TTTTCGGCCACCGCTAACCTGTCTTTAACTGCTTTTAAACCAATATTTATAACCTTG 540

541  TTTTAAACAGGGCTGCGCGCTGTGCGCGTACCGCGGACCGCGAAGGGGGTGCCTCCC 600
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541  TTTTAAACAGGGCTGCGCGCTGTGCGCGTACCGCGGACCGCGAAGGGGGTGCCTCCC 600

601  CTTCTCGAACCTTCCCGAAAGATATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660
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601  CTTCTCGAACCTTCCCGAAAGATATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660

661  AATACGGCATCAGGGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTT 720
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661  AATACGGCATCAGGGCTCTTCCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTT 720

721  CGCTCGCGAGCGGTATCAGCTCACTCAAAGGGCGTAATACGCTTATCCACAGATCA 780
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721  CGCTCGCGAGCGGTATCAGCTCACTCAAAGGGCGTAATACGCTTATCCACAGATCA 780

781  GGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 840
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781  GGGGATAACCGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 840

841  AAGGCCGCGTGTGCTGGCGTTTTCATAGGCTCCGCGCGCGCTGACGAGCATCAAAAAT 900
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841  AAGGCCGCGTGTGCTGGCGTTTTCATAGGCTCCGCGCGCGCTGACGAGCATCAAAAAT 900

901  CGACGCTCAAGTCAGAGTGGCGAAACCGCACAGGACTATAAGATACACGAGGCTTCCC 960
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901  CGACGCTCAAGTCAGAGTGGCGAAACCGCACAGGACTATAAGATACACGAGGCTTCCC 960

961  CTTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCGCGTTACCGGATACCTGTCC 1020
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961  CTTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCCCTCGCGTTACCGGATACCTGTCC 1020

1021  GCCTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGCTAGGTATCTCAGT 1080
    |||||
1021  GCCTTCTCCCTTCGGGAAAGCGTGGCGCTTCTCATAGCTCAGCTGCTAGGTATCTCAGT 1080

1081  TCGGTGTAGTGTGCTTCCGCTTCAAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCGAC 1140
    |||||
1081  TCGGTGTAGTGTGCTTCCGCTTCAAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCGAC 1140

1141  CGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCCGGTAAGACACGACTTATCG 1200
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Db	1141		CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAACACAGCACTTATCG	1200
Qy	1201		CCACTGGCAGAGCCTTCTACCAATAATCCGGATAAACCCAGCGAAACCAATTGAGGTGAT	1260
Db	1201		CCACTGGCAGAGCCTTCTACCAATAATCCGGATAAACCCAGCGAAACCAATTGAGGTGAT	1260
Qy	1261		AGGTAAAGATTATACCGAGGTATGAACACGAGAAATGGACCTTTACAGAAATTAATCTATGA	1320
Db	1261		AGGTAAAGATTATACCGAGGTATGAACACGAGAAATGGACCTTTACAGAAATTAATCTATGA	1320
Qy	1321		AGGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGCGAGATTG	1380
Db	1321		AGGCCATATTTAAAAAGCTACCAAGACGAAGAGATGAAGAGGATGAGGAGGCGAGATTG	1380
Qy	1381		CTTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAAAGATATCGCG	1440
Db	1381		CTTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAAAGATATCGCG	1440
Qy	1441		TATCTAAGGATTTTCAGGGGCAAGGCATAGCAGCGGCTTATCAATATATCTATAGAAT	1500
Db	1441		TATCTAAGGATTTTCAGGGGCAAGGCATAGCAGCGGCTTATCAATATATCTATAGAAT	1500
Qy	1501		GGGCAAAAGCATAAAACTTGCAATGGAATAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Db	1501		GGGCAAAAGCATAAAACTTGCAATGGAATAATGCTTTGAAACCCAGGACAAATAACCTTATAG	1560
Qy	1561		CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCGTGCATACTATGTTATACG	1620
Db	1561		CTTTGTAATTTCTACCAAAATTTGGTTTCAAAATCGGCTCGTGCATACTATGTTATACG	1620
Qy	1621		CCAACTTTGAAACAACTTTGAAAGAGCTGTTTCTGGTATTTAAGCTTTTGAAGTGCAG	1680
Db	1621		CCAACTTTGAAACAACTTTGAAAGAGCTGTTTCTGGTATTTAAGCTTTTGAAGTGCAG	1680
Qy	1681		GGAACTGTAATGGAGTTCGTCTGTTTAAATAGCTTCTTGGGGTATCTTTAAATACT	1740
Db	1681		GGAACTGTAATGGAGTTCGTCTGTTTAAATAGCTTCTTGGGGTATCTTTAAATACT	1740
Qy	1741		GTAGAAAAGAGAAAGGAAATAATAATGGCTTAAATGAGAAATATCACCGAAATGAAAA	1800
Db	1741		GTAGAAAAGAGAAAGGAAATAATAATGGCTTAAATGAGAAATATCACCGAAATGAAAA	1800
Qy	1801		ACTGATCGAAAATACCGCTCGTAAAGATACCGAAGGATGTCCTCTGCTAAGGTATA	1860
Db	1801		ACTGATCGAAAATACCGCTCGTAAAGATACCGAAGGATGTCCTCTGCTAAGGTATA	1860
Qy	1861		TAACTGCTGGGAGAAAATGAAAAACCTATATTTAAAAATGACCGACAGCCGGTATAAAG	1920
Db	1861		TAACTGCTGGGAGAAAATGAAAAACCTATATTTAAAAATGACCGACAGCCGGTATAAAG	1920
Qy	1921		GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTTGGCTGGAAAGGAAAGCTGCC	1980
Db	1921		GACCACCTATGATGTGAAACGGGAAAAGGACATGATGCTTGGCTGGAAAGGAAAGCTGCC	1980
Qy	1981		TGTTCCAAAGGTCCTGCATTTGAAACGCGATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981		TGTTCCAAAGGTCCTGCATTTGAAACGCGATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041		GGCCGATGGGCTCTTTGCTCGGAAGAGTATGAAGATGAAACAAAGCCCTGAAAAAGATTAT	2100
Db	2041		GGCCGATGGGCTCTTTGCTCGGAAGAGTATGAAGATGAAACAAAGCCCTGAAAAAGATTAT	2100
Qy	2101		CGAGCTGATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTGCCCTA	2160
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Qy	2161		TACCAATAGCTTACACAGCCGCTTAGCGGATTCGATTAATCTTACTGTAATACCATCTGGC	2220
Db	2161		TACCAATAGCTTACACAGCCGCTTAGCGGATTCGATTAATCTTACTGTAATACCATCTGGC	2220
Qy	2221		CGATGTGGATTTGCGAAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
Db	2221		CGATGTGGATTTGCGAAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280

Db	2221		CGATGTGGATTTGCGAAAACCTGGGAAGAGACACTCCATTTAAAGATCCGCGCAGCTGTA	2280
Qy	2281		TGATTTTTTAAAGACGGAAAAGCCCGAAGAGAACTTGTCTTTTCCACGGCAGCTGGG	2340
Db	2281		TGATTTTTTAAAGACGGAAAAGCCCGAAGAGAACTTGTCTTTTCCACGGCAGCTGGG	2340
Qy	2341		AGACACAAACATCTTTTGTGAAAAGATGGCAAAGTAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Db	2341		AGACACAAACATCTTTTGTGAAAAGATGGCAAAGTAAGTGGCTTTTATTTGATCTTGGGAGAAG	2400
Qy	2401		CGCAGGGCGGACAAAGTGTATGCAATTCGCTTCTCGCTCCGCTCGATCAGGAGGATAT	2460
Db	2401		CGCAGGGCGGACAAAGTGTATGCAATTCGCTTCTCGCTCCGCTCGATCAGGAGGATAT	2460
Qy	2461		CGGGGAGAACAGTATGTCAGACTATTTTGTACTTCTGGGATCAAGCTCTATTGGGA	2520
Db	2461		CGGGGAGAACAGTATGTCAGACTATTTTGTACTTCTGGGATCAAGCTCTATTGGGA	2520
Qy	2521		GAAAAATAAATATTTATTTTACTGGATGAAATTTTGTAGTACCTAGATGTGGCGCAACG	2580
Db	2521		GAAAAATAAATATTTATTTTACTGGATGAAATTTTGTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581		ATGCCGGGACAAAGCAGGACCGCACTTCTTCCGATCAAGTGTTTTGGCTCTCAGG	2640
Db	2581		ATGCCGGGACAAAGCAGGACCGCACTTCTTCCGATCAAGTGTTTTGGCTCTCAGG	2640
Qy	2641		CGAGGCCCAACGCAAGTATTTTGGCAAGGGTTCGCTGTTTTCGTGAGGGCAAGATTC	2700
Db	2641		CGAGGCCCAACGCAAGTATTTTGGCAAGGGTTCGCTGTTTTCGTGAGGGCAAGATTC	2700
Qy	2701		GGAATACCAAGTACGAGAAGGACGGCCAGACGGCTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701		GGAATACCAAGTACGAGAAGGACGGCCAGACGGCTCTACGGGACCGACTTCATTGCCGATA	2760
Qy	2761		AGTGGAATATCTGGACACAAAGGACCAAGGGGTCAAATCAGGAATTAAGGCAATTC	2820
Db	2761		AGTGGAATATCTGGACACCAAGGACCAAGGGGTCAAATCAGGAATTAAGGCAATTC	2820
Qy	2821		CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGGACGTTTGACCGGA	2880
Db	2821		CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGTGAATGAATCGGACGTTTGACCGGA	2880
Qy	2881		AGGCATACAGGCAAGAACTGATCGACCGGGGTTTTCCGCGAGGATGCCGAAACCATCG	2940
Db	2881		AGGCATACAGGCAAGAACTGATCGACCGGGGTTTTCCGCGAGGATGCCGAAACCATCG	2940
Qy	2941		CAAGCCGACCGTATCGTGGTGGCCCGCGGAAACCTTCCAGTCCGTCGATGGTCC	3000
Db	2941		CAAGCCGACCGTATCGTGGTGGCCCGCGGAAACCTTCCAGTCCGTCGATGGTCC	3000
Qy	3001		AGCAAGCTACGGCCAAAGATCGAGCGGACAGCGTGCAACTGGCTCCCTCGCTGCCCCG	3060
Db	3001		AGCAAGCTACGGCCAAAGATCGAGCGGACAGCGTGCAACTGGCTCCCTCGCTGCCCCG	3060
Qy	3061		CGCCATCGGCGCGCTGAGGAGCTTTCGCTCGTCTCGAAACAGGAGGCGGAGTTGGCGA	3120
Db	3061		CGCCATCGGCGCGCTGAGGAGCTTTCGCTCGTCTCGAAACAGGAGGCGGAGTTGGCGA	3120
Qy	3121		AGTCGATGACCATCGACACCGGAGGAACTATGACGACCAAGAGAGGAAACCGCGGCG	3180
Db	3121		AGTCGATGACCATCGACACCGGAGGAACTATGACGACCAAGAGAGGAAACCGCGGCG	3180
Qy	3181		AGGACCTGGCAAAACAGGTTCAGCGAGGCAAGCGCGCTTGTCTGAAACACACGAAGC	3240
Db	3181		AGGACCTGGCAAAACAGGTTCAGCGAGGCAAGCGCGCTTGTCTGAAACACACGAAGC	3240
Qy	3241		AGCAGATCAAGGAAATGACGCTTTCTTGTTCGATATTCGCCGTGGCCGACACGATGC	3300
Db	3241		AGCAGATCAAGGAAATGACGCTTTCTTGTTCGATATTCGCCGTGGCCGACACGATGC	3300
Qy	3301		GAGCGATGCCAAACGACACAGGCGCGCTCTGCCCCCTGTTTCAACCGCGCAACAGAAATCC	3360
Db	3301		GAGCGATGCCAAACGACACAGGCGCGCTCTGCCCCCTGTTTCAACCGCGCAACAGAAATCC	3360

Qy 3361 CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCACCAAGGACGTGAAGATCACCT 3420  
Db CGCGGAGGCGCTGCAAAACAAGGTCAATTTTCCACGTCACCAAGGACGTGAAGATCACCT 3420  
Qy 3421 ACACCGGCTCGAGCTCGCGGCGCAGATACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480  
Db ACACCGGCTCGAGCTCGCGGCGCAGATACGAACTGGTGTGGCAGCAGGTGTGGAGT 3480  
Qy 3481 ACAGGAGCGCACCCCTATCGCGAGCGCATCACTTCACGTTCTACGAGCTTTGCCAGG 3540  
Db ACAGGAGCGCACCCCTATCGCGAGCGCATCACTTCACGTTCTACGAGCTTTGCCAGG 3540  
Qy 3541 ACTGGGCTGGTCAATCAATGGCCGGTATTACAGAGGCGGAGGAATGCTGTGCGGCC 3600  
Db ACTGGGCTGGTCAATCAATGGCCGGTATTACAGAGGCGGAGGAATGCTGTGCGGCC 3600  
Qy 3601 TACAGGCGAGCGGATGGGCTTACGTCGACCGCTGTGGGACCTTGGAAATCGGTGCGC 3660  
Db TACAGGCGAGCGGATGGGCTTACGTCGACCGCTGTGGGACCTTGGAAATCGGTGCGC 3660  
Qy 3661 TGCTGCACCGCTTCCGCGTCTCGACCGTGGCAAGAAACGTCCTCGTTCAGGTCCTGA 3720  
Db TGCTGCACCGCTTCCGCGTCTCGACCGTGGCAAGAAACGTCCTCGTTCAGGTCCTGA 3720  
Qy 3721 TCAGCAGGAAATCGTCTGCTGTTGCTGCGGACCACTACACGAAATTCATATGGGAGA 3780  
Db TCAGCAGGAAATCGTCTGCTGTTGCTGCGGACCACTACACGAAATTCATATGGGAGA 3780  
Qy 3781 AGTACCGAAGCTGTGCCAGCGGCGGACGGATGTTTGGACTATTTTCAGTTCGACCGGG 3840  
Db AGTACCGAAGCTGTGCCAGCGGCGGACGGATGTTTGGACTATTTTCAGTTCGACCGGG 3840  
Qy 3841 AGCGCTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACACCGCG 3900  
Db AGCGCTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGATCGGATTCACACCGCG 3900  
Qy 3901 TGAAGAAGTGGCGGAGCGGTGCGGAAGCTTCCGAGGAGGCGGCGCTGG 3960  
Db TGAAGAAGTGGCGGAGCGGTGCGGAAGCTTCCGAGGAGGCGGCGCTGG 3960  
Qy 3961 TGAACACGCTGGGTCAATGATGACCTGTGTGATTTGCGGAGCTGCGGAGCTGTT 4020  
Db TGAACACGCTGGGTCAATGATGACCTGTGTGATTTGCGGAGCTGCGGAGCTGTT 4020  
Qy 4021 CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTTTACTGGCATTTCTAGTTACGCTTT 4080  
Db CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTTTACTGGCATTTCTAGTTACGCTTT 4080  
Qy 4081 CTGATGGGCTGCCTGTATCAGTGGTGATTTTGTGCGGAGCTGCCGTCGGGAGCTGTT 4140  
Db CTGATGGGCTGCCTGTATCAGTGGTGATTTTGTGCGGAGCTGCCGTCGGGAGCTGTT 4140  
Qy 4141 GGCTGGTGTGGCAGATATATGTTGGTGAACAAATTTGACGCTTAGCAACTTAATA 4200  
Db GGCTGGTGTGGCAGATATATGTTGGTGAACAAATTTGACGCTTAGCAACTTAATA 4200  
Qy 4201 ACACATTGGGAGCTTTTAAATGATGATGTTGGGCTATCCCCGGGGGATATCCATAGCCCG 4260  
Db ACACATTGGGAGCTTTTAAATGATGATGTTGGGCTATCCCCGGGGGATATCCATAGCCCG 4260  
Qy 4261 ATCTAGTAACATAATGACCGCGGATATTTATCTAGTTTTCGGGCTATATTTTG 4320  
Db ATCTAGTAACATAATGACCGCGGATATTTATCTAGTTTTCGGGCTATATTTTG 4320  
Qy 4321 TTTTCTATCGGTTAAATGATATATGTTGGGACTTAATATAAAACCCCATCTATA 4380  
Db TTTTCTATCGGTTAAATGATATATGTTGGGACTTAATATAAAACCCCATCTATA 4380  
Qy 4381 AATAAGCTATGATACATGTTTAAATATATGATGCTTAACGTTAAATCAACAGAAATAT 4440  
Db AATAAGCTATGATACATGTTTAAATATATGATGCTTAACGTTAAATCAACAGAAATAT 4440

Qy 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTATTCCTCAATG 4500  
Db 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTAAGAACTTTATTCCTCAATG 4500  
Qy 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCGA 4533  
Db 4501 TTTGAACGATCGTTCGTCGAGCTATGGGCCCA 4533

RESULT 7  
US-09-845-064-6  
; Sequence 6, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 6016  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pmrT1122  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus coding for two proteins, p285 and p382,  
; OTHER INFORMATION: enabling the increase in the rate of replication  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4105)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4560)..(5556)  
; OTHER INFORMATION: Wild type NPT II gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (5557)..(5770)  
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5770)..(5836)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5836)..(6009)  
; OTHER INFORMATION: T-DNA right border

US-09-845-064-6

Query Match	94.3%;	Score 4531.4;	DB 10;	Length 6016;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4532;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	CCGGCGTGGTTGCCCTCGCGCTGGCGTGGCGGCGGCTCTATGGCCCTGCAAAACGCGCCAG	60	
Db	1	CCGGCGTGGTTGCCCTCGCGCTGGCGTGGCGGCGGCTCTATGGCCCTGCAAAACGCGCCAG	60	
Qy	61	AAACCGCGTCGAAGCCGTGTGCGAGACAACCGCGGCCCGCGGCTGTGTGGATACCTCGCGG	120	
Db	61	AAACCGCGTCGAAGCCGTGTGCGAGACAACCGCGGCCCGCGGCTGTGTGGATACCTCGCGG	120	
Qy	121	AAAACTTGGCCCTCACTGACAGATGAGGGGGGAGCGTTGACACTTGAAGGGCGCGACTCAC	180	
Db	121	AAAACTTGGCCCTCACTGACAGATGAGGGGGGAGCGTTGACACTTGAAGGGCGCGACTCAC	180	
Qy	181	CCGGCGCGGGTGTGACAGATGAGGGGCGAGGCTCGATTTCGGCCGCGCACGTGGAGCTGGC	240	
Db	181	CCGGCGCGGGTGTGACAGATGAGGGGCGAGGCTCGATTTCGGCCGCGCACGTGGAGCTGGC	240	
Qy	241	CAGCCTCGCAAAATCGGGCAAAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGGA	300	
Db	241	CAGCCTCGCAAAATCGGGCAAAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGGA	300	
Qy	301	CAAGCCTGGGGATAAGTGCCTCGCGGTATTGACACTTTGAGGGGCGCGACTTACTGACAGAT	360	
Db	301	CAAGCCTGGGGATAAGTGCCTCGCGGTATTGACACTTTGAGGGGCGCGACTTACTGACAGAT	360	
Qy	361	GAGGGCGCGATCCTTGACACTTGAGGGGCGAGTGTGTACAGATGAGGGGCGCACCTAT	420	
Db	361	GAGGGCGCGATCCTTGACACTTGAGGGGCGAGTGTGTGTACAGATGAGGGGCGCACCTAT	420	
Qy	421	TGACATTTGAGGGGCTGTCCACAGCGCAGAAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480	
Db	421	TGACATTTGAGGGGCTGTCCACAGCGCAGAAAATCCAGCATTTGCAAGGGTTTCGCGCCGT	480	
Qy	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTTTAAACCAATATTTATAACCTTG	540	
Db	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAAACCTGCTTTTTTAAACCAATATTTATAACCTTG	540	
Qy	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAAGGGGGGTGCCCCC	600	
Db	541	TTTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGCACCGCGAAGGGGGGTGCCCCC	600	
Qy	601	CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660	
Db	601	CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660	
Qy	661	AAATACCGCATCAGGCGCTCTTCGCTTCCTCGTCTCACTGACTCGCTGCGCTCGGTGCTT	720	
Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCCTCGTCTCACTGACTCGCTGCGCTCGGTGCTT	720	
Qy	721	CGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGGTTTATCCACAGAAATCA	780	
Db	721	CGGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTATACGGTTTATCCACAGAAATCA	780	
Qy	781	GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGGAAACCGTAAA	840	
Db	781	GGGGATAACCGAGGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGGAAACCGTAAA	840	
Qy	841	AAGCGCGGTGCTGGCGTTTTCATAGGCTCGCCCCCTGACGAGCATCACAAAAT	900	
Db	841	AAGCGCGGTGCTGGCGTTTTCATAGGCTCGCCCCCTGACGAGCATCACAAAAT	900	
Qy	901	CGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAGATACACGAGCGTTTCCC	960	
Db	901	CGACGCTCAAGTCAGAGGTGCGGAAACCCGACAGGACTATAAGATACACGAGCGTTTCCC	960	
Qy	961	CCTCGAAGCTCCCTGTCGCTCTCTCTTTCGACCTGCGCTTACCGATACCTGTCC	1020	
Db	961	CCTCGAAGCTCCCTGTCGCTCTCTCTTTCGACCTGCGCTTACCGATACCTGTCC	1020	

Qy	2101	CGAGCTGTATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTCCTTA	2160
Db	2101	CGAGCTGTATGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTTCCTTA	2160
Qy	2161	TACCAATAGCTTACACAGCCGCTTAGCGAATTGGATTACTTACTGAATACGATCTGGC	2220
Db	2161	TACCAATAGCTTACACAGCCGCTTAGCGAATTGGATTACTTACTGAATACGATCTGGC	2220
Qy	2221	CGATGTGGATTGCGAAATCGGGAAGAGACACTCCATTTAAAGATCCGGCGGAGCTGTA	2280
Db	2221	CGATGTGGATTGCGAAATCGGGAAGAGACACTCCATTTAAAGATCCGGCGGAGCTGTA	2280
Qy	2281	TGATTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTCCACGCGACCTGGG	2340
Db	2281	TGATTTTAAAGACGGAAAGCCCGAAGAGAACTTGTCTTTCCACGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTCTGGAAGATGCCAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTCTGGAAGATGCCAAGTAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Qy	2401	CGGCAAGGCGGACAAAGTGGTATGACATTTGCCCTTCGGTCCGGTCCGATCAGGGAGGATAT	2460
Db	2401	CGGCAAGGCGGACAAAGTGGTATGACATTTGCCCTTCGGTCCGGTCCGATCAGGGAGGATAT	2460
Qy	2461	CGGGAAAGAACAGTATGTCGAGCTATTTTGTACTTACTGGGATCAAGCCTGATTGGGA	2520
Db	2461	CGGGAAAGAACAGTATGTCGAGCTATTTTGTACTTACTGGGATCAAGCCTGATTGGGA	2520
Qy	2521	GAATAATAATATTTATTTACTTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Db	2521	GAATAATAATATTTATTTACTTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581	ATGCCGCGCAACAGCAGGCGCACCGCACTTCTTCGCACTCAAGTGTTCCTCAGG	2640
Db	2581	ATGCCGCGCAACAGCAGGCGCACCGCACTTCTTCGCACTCAAGTGTTCCTCAGG	2640
Qy	2641	CCGAGGCCCAAGTATTTGGGCAAGGGTTCGCTGGTATTCGTCAGGCGCAAGATTC	2700
Db	2641	CCGAGGCCCAAGTATTTGGGCAAGGGTTCGCTGGTATTCGTCAGGCGCAAGATTC	2700
Qy	2701	GGATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Db	2701	GGATACCAAGTACGAGAAGACGGCCAGACGGTCTACGGGACCGACTTCATTGCCGATA	2760
Qy	2761	AGGTGGATTATCTGGACACCAAGSCACAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761	AGGTGGATTATCTGGACACCAAGSCACAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Qy	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA	2880
Db	2821	CCCCGGCTGAGTCGGGGCAATCCCGCAAGGAGGGTGAATGAATCGGACGTTTTGACCGGA	2880
Qy	2881	AGGCATACAGCAAGAACTGATCGACCGGGGTTTTCCGGCGAGGATGCCGAACCATCG	2940
Db	2881	AGGCATACAGCAAGAACTGATCGACCGGGGTTTTCCGGCGAGGATGCCGAACCATCG	2940
Qy	2941	CAAGCCGACCGTATCGGTGCGCCCGGAAACCTTCCAGTCCGTCCGGTTCGATGGTCC	3000
Db	2941	CAAGCCGACCGTATCGGTGCGCCCGGAAACCTTCCAGTCCGTCCGGTTCGATGGTCC	3000
Qy	3001	AGCAAGCTACGGCCAAAGATCGAGCGCACGCTGCAACTGGCTCCCGCTGCCCTGCCCG	3060
Db	3001	AGCAAGCTACGGCCAAAGATCGAGCGCGACGCTGCAACTGGCTCCCGCTGCCCTGCCCG	3060
Qy	3061	CGCCATCGGCGCGCTGGAGGTTTCGCTCTCGAAACAGGAGCGGCAAGTTTGGCGA	3120
Db	3061	CGCCATCGGCGCGCTGGAGGTTTCGCTCTCGAAACAGGAGCGGCAAGTTTGGCGA	3120
Qy	3121	AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGACGGAACCCCGCGCG	3180
Db	3121	AGTCGATGACCATCGACCGGAGGAACTATGACGACCAAGACGGAACCCCGCGCG	3180
Qy	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGAGGCGCGTTCCTGTAACACACGGAAGC	3240

Db	3181	AGGACCTGGCAAAACAGGTCAGCGAGGCCAAGAGGCGCGTTCCTGTAACACACGGAAGC	3240
Qy	3241	AGCAGATCAAGGAAATGACAGCTTTCTTGTTCGATATTGCGCGCGTGGCCGACACGATGC	3300
Db	3241	AGCAGATCAAGGAAATGACAGCTTTCTTGTTCGATATTGCGCGCGTGGCCGACACGATGC	3300
Qy	3301	GAGCGATGCCAAACGACACAGCGCCGCTCTGCCCTGTTTACCACGCGCAACAAGAAAAATCC	3360
Db	3301	GAGCGATGCCAAACGACACAGCGCCGCTCTGCCCTGTTTACCACGCGCAACAAGAAAAATCC	3360
Qy	3361	CGCGGAGGCGCTGCAAAAACAAGTCAATTTTCCACGTCAAACAGGACGTAAGATCACCT	3420
Db	3361	CGCGGAGGCGCTGCAAAAACAAGTCAATTTTCCACGTCAAACAGGACGTAAGATCACCT	3420
Qy	3421	ACACCGCGCTCGAGCTCGGGCCGACGATGACCAATGCTGCTGGTGGCAGCAGGTGTTGAGT	3480
Db	3421	ACACCGCGCTCGAGCTCGGGCCGACGATGACCAATGCTGCTGGTGGCAGCAGGTGTTGAGT	3480
Qy	3481	ACGCGAAGCGCACCCCTATCGCGAGCCGATCACTTTCAGCTTCTACGAGCTTTGCCAGG	3540
Db	3481	ACGCGAAGCGCACCCCTATCGCGAGCCGATCACTTTCAGCTTCTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGGTCCGATCAATGCGCGGATTTACACGAAGCCGAGGAATGCTGTCGCGCC	3600
Db	3541	ACCTGGGCTGGTCCGATCAATGCGCGGATTTACACGAAGCCGAGGAATGCTGTCGCGCC	3600
Qy	3601	TACAGGAGCGGCGATGGGCTTCACTCCGACCGCTTGGGCACTTGGAAATCGGTGTCG	3660
Db	3601	TACAGGAGCGGCGATGGGCTTCACTCCGACCGCTTGGGCACTTGGAAATCGGTGTCG	3660
Qy	3661	TGCTGCACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGCTCCCGTTGCGAGGCTCTGA	3720
Db	3661	TGCTGCACCGCTTCCGCGTCTCGGACCGTGGCAAGAAACGCTCCCGTTGCGAGGCTCTGA	3720
Qy	3721	TCGACGAGGAAATCGTCTGCTGTTGCTGGCCACCACTACACGAAATTCATATGGGAGA	3780
Db	3721	TCGACGAGGAAATCGTCTGCTGTTGCTGGCCACCACTACACGAAATTCATATGGGAGA	3780
Qy	3781	AGTACCGCAGCTGTCGCCGACGGCCGAGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAGCTGTCGCCGACGGCCGAGGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCGGTACCGCTCAAGCTGGAAAACCTTCCGCTCATGTGCGGATCGGATTCACACCGCG	3900
Db	3841	AGCGGTACCGCTCAAGCTGGAAAACCTTCCGCTCATGTGCGGATCGGATTCACACCGCG	3900
Qy	3901	TGAAGAAGTGGCGCAGCAGGTCCGGCAGAGCTCGGCGAAGCTTCGAGGCGAGCGGCTGG	3960
Db	3901	TGAAGAAGTGGCGCAGCAGGTCCGGCAGAGCTCGGCGAAGCTTCGAGGCGAGCGGCTGG	3960
Qy	3961	TGGAAACACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACCTAGGGCTTTGCGGGT	4020
Db	3961	TGGAAACACGCTGGGTCAATGATGACCTGGTGCATTTGCAAAACCTAGGGCTTTGCGGGT	4020
Qy	4021	CAGTTCGCGCTGGGGTTTACGACGCGCTTTTACTGGGCATTTCTTAGGTTCACGCTTT	4080
Db	4021	CAGTTCGCGCTGGGGTTTACGACGCGCTTTTACTGGGCATTTCTTAGGTTCACGCTTT	4080
Qy	4081	CTGATGGGCTGCTGATCGAGTGGTGAATTTGTCGCGAGCTCCCGTTCGGGAGCTGTTT	4140
Db	4081	CTGATGGGCTGCTGATCGAGTGGTGAATTTGTCGCGAGCTCCCGTTCGGGAGCTGTTT	4140
Qy	4141	GGCTGCTGGTGGCAGGATATATTGTTGGTGAACAAATTTGACGCTTAGACAACCTTAATA	4200
Db	4141	GGCTGCTGGTGGCAGGATATATTGTTGGTGAACAAATTTGACGCTTAGACAACCTTAATA	4200
Qy	4201	ACACATTTGGGAGCTTTTAAATGCTACTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Db	4201	ACACATTTGGGAGCTTTTAAATGCTACTGGGGCTATCCCGGGGGATATCCATAGGCCCG	4260
Qy	4261	ATCTAGTAACATAATGACACCGCGCGGATAATTTTATCTCTAGTTTTCGCGCTATATTTTG	4320

Db 4261 ATCTAGTAACATAATGACACCGCGCGATAATTATTCCTAGTTTGGCGCTATATTTTG 4320  
Qy 4321 TTTTCTATCGGTAATTAATGTAATAATTGGGGACTCTAATCATATAAAACCCATCTCATTA 4380  
Db 4321 TTTTCTATCGGTAATTAATGTAATAATTGGGGACTCTAATCATATAAAACCCATCTCATTA 4380  
Qy 4381 AATAACGTCATGCATTACATGTTAAATTATTACATGCTTTAAACGTAATTCACAGAAATTA 4440  
Db 4381 AATAACGTCATGCATTACATGTTAAATTATTACATGCTTTAAACGTAATTCACAGAAATTA 4440  
Qy 4441 ATGATATATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATTGCAAAATG 4500  
Db 4441 ATGATATATCATCGCAACCGCGCAACAGGATTCATCTTAAGAACTTTATTGCAAAATG 4500  
Qy 4501 TTTGAACGATCGTTCGTGCGAGCTATGGGCCGA 4533  
Db 4501 TTTGAACGATCGTTCGTGCGAGCTATGGGCCCAA 4533

RESULT 8

US-09-845-064-5  
; Sequence 5, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; FILE REFERENCE: Synvec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 6017  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pMRT1121  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1)-(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)-(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)-(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)-(4098)  
; OTHER INFORMATION: Trifa locus coding for two proteins, P285 and P382,  
; OTHER INFORMATION: enabling the increase in the rate of replication  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)-(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)-(4559)  
; OTHER INFORMATION: No. US20030175976Ala1line synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4560)-(5556)  
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase  
; OTHER INFORMATION: and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc\_difference

; LOCATION: (5559)  
; OTHER INFORMATION: BspEI restriction site introduced with respect to  
; OTHER INFORMATION: pMRT1119  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (5557)..(5771)  
; OTHER INFORMATION: No. US20030175976Ala1line synthetase promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5771)..(5837)  
; OTHER INFORMATION: MCS multiple cloning site  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5837)..(6010)  
; OTHER INFORMATION: T-DNA right border  
; US-09-845-064-5  
  
Query Match 94.3%; Score 4531.4; DB 10; Length 6017;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CCGGGCTGTTGCCCTTCGCCGCTGGCGCTGGCGCCCTCTATGGCCCTCGAAACGCGCCAG 60  
Db 1 CCGGGCTGTTGCCCTTCGCCGCTGGCGCTGGCGCCCTCTATGGCCCTCGAAACGCGCCAG 60  
  
Qy 61 AAACGCGTCGAGCCGCTGTCGAGACACCGCGCGCCGCGCTTGTGGATACCTCGCGG 120  
Db 61 AAACGCGTCGAGCCGCTGTCGAGACACCGCGCGCCGCGCTTGTGGATACCTCGCGG 120  
  
Qy 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGCGCGACTCAC 180  
  
Qy 181 CCGGCGCGCTTGA CAGATGAGGGCGAGCTCGATTTCGCCGCGGACGCTGAGCTGGC 240  
Db 181 CCGGCGCGCTTGA CAGATGAGGGCGAGCTCGATTTCGCCGCGGACGCTGAGCTGGC 240  
  
Qy 241 CAGCCTCGCAAAATCGCGGAAACGCTGATTTTACCGAGTTTCCACACAGATGATGGA 300  
Db 241 CAGCCTCGCAAAATCGCGGAAACGCTGATTTTACCGAGTTTCCACACAGATGATGGA 300  
  
Qy 301 CAAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGCGCGACTTACTGACAGAT 360  
Db 301 CAAAGCCTGGGGATAAGTGGCCCTGCGGTATTGACACTTGAGGGCGCGACTTACTGACAGAT 360  
  
Qy 361 GAGGGCGCGATCCTTGA CACTTTGAGGGCGAGTGTCTGACAGATGAGGGCGCACCTAT 420  
Db 361 GAGGGCGCGATCCTTGA CACTTTGAGGGCGAGTGTCTGACAGATGAGGGCGCACCTAT 420  
  
Qy 421 TGACATTTGAGGGGCTGTCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCGCCCGCT 480  
Db 421 TGACATTTGAGGGGCTGTCACAGGCGAGAAATCCAGCATTTTCAAGGGTTTCGCCCGCT 480  
  
Qy 481 TTTTTCGCCACACCGCTAAACCTGCTTTTAACTCTCTTTTAAACCAATATTTATAAACCTTG 540  
Db 481 TTTTTCGCCACACCGCTAAACCTGCTTTTAACTCTCTTTTAAACCAATATTTATAAACCTTG 540  
  
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Db 541 TTTTAAACAGGGCTGCGCCCTGTGCGGTGACCGCGACCGCGAAGGGGGTGCCCCC 600  
  
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Db 661 AAATACCGCATCAGGGCGCTCTCCGCTTCTCCCTCACTGACTCGCTCGGCTCGGTCGT 720  
  
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Db 721 CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGGTAATACGGTTATCCACAGATCA 780



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DB 841 AAGGCCGGTGTCTGCGGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAAT 900  
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3841 AGCCGTACCCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATTCGACCCCGC 3900  
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Qy 4261 ATCTAGTAACATAATGACACCGCGCGGATAATTTATCTAGTTTGGCGCTATATTTTG 4320  
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RESULT 9

US-09-845-064-7  
; Sequence 7, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 6017  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid  
; OTHER INFORMATION: pmr1155  
; FEATURE:  
; NAME/KEY: rep\_origin  
; LOCATION: (1)..(1654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep\_origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus coding for two proteins, p285 and p382,  
; OTHER INFORMATION: enabling the increase in the rate of replication

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
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; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
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; FEATURE:
; NAME/KEY: gene
; LOCATION: (4560)..(5556)
; OTHER INFORMATION: Wild type NPT II gene coding for neomycin
; OTHER INFORMATION: transerase and kanamycin resistance
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; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5771)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5771)..(5837)
; OTHER INFORMATION: MCS multiple cloning site
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5837)..(6010)
; OTHER INFORMATION: T-DNA right border
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US-09-845-064-7

Query Match          94.3%; Score 4531.4; DB 10; Length 6017;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	1861	TAAGCTGGTGGGAGAAATGAAACCTATATTTAAATAAGACGCGGTATTAAGG	1920
Db	1861	TAAGCTGGTGGGAGAAATGAAACCTATATTTAAATAAGACGCGGTATTAAGG	1920
Qy	1921	GACCACTATGATGTGAAACGGGAAAGACATGATCTATGCTGGAAGGAAAGCTGCC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGACATGATCTATGCTGGAAGGAAAGCTGCC	1980
Qy	1981	TGTTCCAAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Db	1981	TGTTCCAAAGGTCTGCACTTTGAAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
Qy	2041	GGCGGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCGGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGATGCGGAGTGCATCAGGCTCTTCACTCCATCGACATATCGGATTGTCCTTA	2160
Db	2101	CGAGCTGATGCGGAGTGCATCAGGCTCTTCACTCCATCGACATATCGGATTGTCCTTA	2160
Qy	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTAGACAGCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTGCGAAACCTGGGAAGAGACATCTCCATTTAAAGATCCGCGGAGCTGTA	2280
Db	2221	CGATGTGGATTGCGAAACCTGGGAAGAGACATCTCCATTTAAAGATCCGCGGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACGAAAGCCGGAAGGAACTTGTCTTTTCCACGCGCACTGGG	2340
Db	2281	TGATTTTTTAAAGACGAAAGCCGGAAGGAACTTGTCTTTTCCACGCGCACTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTGAAAGATGGCAAGTAAAGTGGCTTTATTGATCTTGGGAGAAG	2400
Qy	2401	CGGAGGGCGGACAAGTGGTATGACATTTGCCCTTCTGGCTCCGGTCGATCAGGGAGGATAT	2460
Db	2401	CGGAGGGCGGACAAGTGGTATGACATTTGCCCTTCTGGCTCCGGTCGATCAGGGAGGATAT	2460
Qy	2461	CGGGAGAAACAGTATGTCGAGCTATTTTGTAGCTTACTGGGGATCAAGCTGATTGCGGA	2520
Db	2461	CGGGAGAAACAGTATGTCGAGCTATTTTGTAGCTTACTGGGGATCAAGCTGATTGCGGA	2520
Qy	2521	GAAATAAATATTTATTTTACTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Db	2521	GAAATAAATATTTATTTTACTGGATGAATTTGTTTAGTACCTAGATGTGGCGCAACG	2580
Qy	2581	ATGCCGGCGCAACAGCAGAGCGCACCGACTTCTTCCGCAATCAAGTGTGTTGGCTCTCAGG	2640
Db	2581	ATGCCGGCGCAACAGCAGAGCGCACCGACTTCTTCCGCAATCAAGTGTGTTGGCTCTCAGG	2640
Qy	2641	CCGAGGCCACGCAAGTATTTTGGCAAGGGTCTGCTGTTATTCGTGCAGGGCAAGATTTC	2700
Db	2641	CCGAGGCCACGCAAGTATTTTGGCAAGGGTCTGCTGTTATTCGTGCAGGGCAAGATTTC	2700
Qy	2701	GGAATACCAAGTACGAGAAGACGGCCAGACGGCTACGGGACCGACTTCAATTGCCGATA	2760
Db	2701	GGAATACCAAGTACGAGAAGACGGCCAGACGGCTACGGGACCGACTTCAATTGCCGATA	2760
Qy	2761	AGGTGGATTATCTGGACACCAAGGACACGAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820
Db	2761	AGGTGGATTATCTGGACACCAAGGACACGAGCGGGTCAAAATCAGGAATAAGGGCACATTG	2820

Qy	2821	CCCCGGCTGAGTCCGGGCAATCCCACAAGGAGGTGAATGAATCGACGTTTTCACCGGA	2880
Db	2821	CCCCGGCTGAGTCCGGGCAATCCCACAAGGAGGTGAATGAATCGACGTTTTCACCGGA	2880
Qy	2881	AGGCATACAGGCAAGAACTGATCGACCGGGGTTTTTCCCGCAGGATCCGGAACCATCG	2940
Db	2881	AGGCATACAGGCAAGAACTGATCGACCGGGGTTTTTCCCGCAGGATCCGGAACCATCG	2940
Qy	2941	CAAAGCCGACCGTCAATGCGTGGCCCGGAAACCTTCCAGTCCGTCGCTCGATGGTCC	3000
Db	2941	CAAAGCCGACCGTCAATGCGTGGCCCGGAAACCTTCCAGTCCGTCGATGGTCC	3000
Qy	3001	AGCAAGCTACGGCAAGATCGAGCGCAGACAGCGTGAACCTGCGTCCCCCTGCGCTCCCG	3060
Db	3001	AGCAAGCTACGGCAAGATCGAGCGCAGACAGCGTGAACCTGCGTCCCCCTGCGCTCCCG	3060
Qy	3061	CGCCATCGGCGCGCTGGAGCGTTCCGTCGTCCTCGAAACAGGAGCGGAGGTTTGGCGA	3120
Db	3061	CGCCATCGGCGCGCTGGAGCGTTCCGTCGTCCTCGAAACAGGAGCGGAGGTTTGGCGA	3120
Qy	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGAAACCCCGCGCG	3180
Db	3121	AGTCGATGACCATCGACACGCGAGGAACTATGACGACCAAGAGCGAAACCCCGCGCG	3180
Qy	3181	AGGACCTGGCAAAACAGGTACAGCGGCCAAGCAGCCCGCTTGTGAAACACACGAAGC	3240
Db	3181	AGGACCTGGCAAAACAGGTACAGCGGCCAAGCAGCCCGCTTGTGAAACACACGAAGC	3240
Qy	3241	AGCAGATCAAGGAATGCGAGCTTCTTGTTCGATATTGGCCCGTGGCCGACACCATGC	3300
Db	3241	AGCAGATCAAGGAATGCGAGCTTCTTGTTCGATATTGGCCCGTGGCCGACACCATGC	3300
Qy	3301	GAGCGATGCCAAACAGACACGGCCCGCTCTGCCCTGTTTCCACCGCGCAACAGAAATCC	3360
Db	3301	GAGCGATGCCAAACAGACACGGCCCGCTCTGCCCTGTTTCCACCGCGCAACAGAAATCC	3360
Qy	3361	CGCGCAGGCGCTGCAAAACAGAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Db	3361	CGCGCAGGCGCTGCAAAACAGAGTCAATTTTCCACGTCAACAAAGGACGTGAAGATCACCT	3420
Qy	3421	ACACCGGCTGAGCTGCGGGCCGACGATGACGAACTGCTGTGGCAGCAGGTGTTGGAGT	3480
Db	3421	ACACCGGCTGAGCTGCGGGCCGACGATGACGAACTGCTGTGGCAGCAGGTGTTGGAGT	3480
Qy	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACCTTTCAGTCTTACGAGCTTTGCCAGG	3540
Db	3481	ACCGAAGCGCACCCCTATCGCGGAGCCGATCACCTTTCAGTCTTACGAGCTTTGCCAGG	3540
Qy	3541	ACCTGGGCTGTCGATCAATGGCCGGTATTACACGAAGCCGAGGAATGCTGTGCGGCC	3600
Db	3541	ACCTGGGCTGTCGATCAATGGCCGGTATTACACGAAGCCGAGGAATGCTGTGCGGCC	3600
Qy	3601	TACAGGCGACGGCGATGGGCTTACGTCGACCGGCTTGGGACCTTGGAAATCGGTGTCGC	3660
Db	3601	TACAGGCGACGGCGATGGGCTTACGTCGACCGGCTTGGGACCTTGGAAATCGGTGTCGC	3660
Qy	3661	TGCTGACACCGCTTCCGCGTCTCGACCGTGGCAAGAAACGTCCTGTTGCGAGGTCCTGA	3720
Db	3661	TGCTGACACCGCTTCCGCGTCTCGACCGTGGCAAGAAACGTCCTGTTGCGAGGTCCTGA	3720
Qy	3721	TCGACGAGGAAATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	3780
Db	3721	TCGACGAGGAAATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	3780
Qy	3781	AGTACCGCAAGCTGTGCGCGACCGGCGGACGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Db	3781	AGTACCGCAAGCTGTGCGCGACCGGCGGACGATGTTTCGACTATTTTCAGCTCCGACCGGG	3840
Qy	3841	AGCGGTACCGCTCAAGCTCGAAACCTTCCGCTCATGTGCGGATCGAATTCACACCGCG	3900
Db	3841	AGCGGTACCGCTCAAGCTCGAAACCTTCCGCTCATGTGCGGATCGAATTCACACCGCG	3900
Qy	3901	TGAAGAGTGGCGGACGAGTGGCGGAGGCTTCCGAAAGAGTTGCGAGGAGCGGCGCTGG	3960

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Db 3901 TGAAGAAAGTGGCGGACAGAGTGGCGAAGCCTGCGAAGAGTTGCGAGGCGAGCGGCTGG 3960
Qy 3961 TGAACACGCGTGGGTCAATGATGACCTGGTGCATTGCAAAACGCTAGGCGCTTGTGGGGT 4020
Db 3961 TGAACACGCGTGGGTCAATGATGACCTGGTGCATTGCAAAACGCTAGGCGCTTGTGGGGT 4020
Qy 4021 CAGTTCGGCTGGGGTTACGACGCCAGCGCTTTACTGCGCATTTCTAGGTGACGCTTT 4080
Db 4021 CAGTTCGGCTGGGGTTACGACGCCAGCGCTTTACTGCGCATTTCTAGGTGACGCTTT 4080
Qy 4081 CTGATGGCGTCCCTGATGACGAGTGGTATTTGTCGCGAGCTGCCGTCGGGGAGCTGTT 4140
Db 4081 CTGATGGCGTCCCTGATGACGAGTGGTATTTGTCGCGAGCTGCCGTCGGGGAGCTGTT 4140
Qy 4141 GGCTGGCTGGTGGCAGGATATATTGCTGTAAACAAATTTGACGCTTAGACAACTTAATA 4200
Db 4141 GGCTGGCTGGTGGCAGGATATATTGCTGTAAACAAATTTGACGCTTAGACAACTTAATA 4200
Qy 4201 ACACATTCGCGAGCTTTTAAATGATCTGGGGCTATCCCCGGGGGATATCCATAGGCCCG 4260
Db 4201 ACACATTCGCGAGCTTTTAAATGATCTGGGGCTATCCCCGGGGGATATCCATAGGCCCG 4260
Qy 4261 ATCTAGTAACATATGACACGCGCGGCGATAATTATCTCTAGTTTGGCGCTATATTTG 4320
Db 4261 ATCTAGTAACATATGACACGCGCGGCGATAATTATCTCTAGTTTGGCGCTATATTTG 4320
Qy 4321 TTTTCTATCCGCTATTAATGTTAAATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380
Db 4321 TTTTCTATCCGCTATTAATGTTAAATTTGCGGAGCTCTAATCATATAAAACCCATCTCAT 4380
Qy 4381 AATAACGTCATGCTATCATATGTTTAAATTTATTTACATGCTTAAACGTAATTTCAACAGAAATTAT 4440
Db 4381 AATAACGTCATGCTATCATATGTTTAAATTTATTTACATGCTTAAACGTAATTTCAACAGAAATTAT 4440
Qy 4441 ATGATAATCATTCGACACCGCGGACAGGATTCATCTTAAGAAACTTTATTCGCAAAATG 4500
Db 4441 ATGATAATCATTCGACACCGCGGACAGGATTCATCTTAAGAAACTTTATTCGCAAAATG 4500
Qy 4501 TTTTGAACGATCGTTTCTGTCGAGCTATGGGCCCGA 4533
Db 4501 TTTTGAACGATCGTTTCTGTCGAGCTATGGGCCCGA 4533
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; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; TITLE OF INVENTION: METHODS OF PRODUCTION
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 6767
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
; OTHER INFORMATION: pMR11175
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1)..(654)
; OTHER INFORMATION: Origin of replication ori RK2
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (655)..(1263)
; OTHER INFORMATION: Origin of replication ori Colei
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; FEATURE:
; NAME/KEY: gene
; LOCATION: (1264)..(2603)
; OTHER INFORMATION: NPT III gene coding for neomycin
; OTHER INFORMATION: phosphotransferase and kanamycin resistance
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2604)..(4098)
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, p285
; OTHER INFORMATION: and p382, enabling the increase in the rate of
; OTHER INFORMATION: replication
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4106)..(4271)
; OTHER INFORMATION: T-DNA left border
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (4272)..(4559)
; OTHER INFORMATION: No. US20030175976Alaline synthetase terminator
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4559)..(5556)
; OTHER INFORMATION: NPT II gene coding for neomycin phosphotransferase
; OTHER INFORMATION: and kanamycin resistance
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (5557)..(5771)
; OTHER INFORMATION: No. US20030175976Alaline synthetase promoter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5771)..(5830)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: (5830)..(6560)
; OTHER INFORMATION: Poly A from 35S ribosome
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6560)..(6587)
; OTHER INFORMATION: MCS multiple cloning site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6587)..(6760)
; OTHER INFORMATION: T-DNA right border
; US-09-845-064-8
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Query Match 94.3%; Score 4531.4; DB 10; Length 6767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTGTTGCCCTCGCGCTGGGCTGGGCGCGCTCTATGGCCCTGCAAAACGCCGCGAG 60
Db 1 CCGGGCTGTTGCCCTCGCGCTGGGCTGGGCGCGCTCTATGGCCCTGCAAAACGCCGCGAG 60

Qy 61 AAACGCGTCGAAGCGCGTGTGCGAGACACCGCGCGCGCGGCTTGTGGATACCTCGCGG 120
Db 61 AAACGCGTCGAAGCGCGTGTGCGAGACACCGCGCGCGCGGCTTGTGGATACCTCGCGG 120

Qy 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Db 121 AAAAATTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180

Qy 181 CCGGCGCGCGGTTGACAGATGAGGGCGAGGCTCGATTTTCGCGCGGCGAGCTGGAGCTGGC 240
Db 181 CCGGCGCGCGGTTGACAGATGAGGGCGAGGCTCGATTTTCGCGCGGCGAGCTGGAGCTGGC 240

Qy 241 CAGCCTCGCAAAATCGCGGAAAAACGCGCTGATTTTACCGAGTTTCCACAGATGATGTGA 300
Db 241 CAGCCTCGCAAAATCGCGGAAAAACGCGCTGATTTTACCGAGTTTCCACAGATGATGTGA 300

Qy 301 CAAGCCTGGGGATAAGTGCCTTCGCGGTATTGACACTTTGAGGGGCGGCGACTTACTGACAGAT 360
Db 301 CAAGCCTGGGGATAAGTGCCTTCGCGGTATTGACACTTTGAGGGGCGGCGACTTACTGACAGAT 360
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Qy	361	GAGGGCGCGATCCTTTGACACTTTGAGGGGAGAGTGTGCAGATGAGGGGCGCACCTAT	420
Db	361	GAGGGCGCGATCCTTTGACACTTTGAGGGGAGAGTGTGCAGATGAGGGGCGCACCTAT	420
Qy	421	TGACATTTGAGGGCTGTCACAGCGAGAAAATCCAGCATTTGCAAGGGTTTCGCCCGT	480
Db	421	TGACATTTGAGGGCTGTCACAGCGAGAAAATCCAGCATTTGCAAGGGTTTCGCCCGT	480
Qy	481	TTTTTCGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAACCTTG	540
Db	481	TTTTTCGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAACCTTG	540
Qy	541	TTTTTAAACAGGGTGCGCCCTGTGCGCTGACCGCGCAGCCGAAAGGGGGTGCCCCC	600
Db	541	TTTTTAAACAGGGTGCGCCCTGTGCGCTGACCGCGCAGCCGCGAAGGGGGTGCCCCC	600
Qy	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660
Db	601	CTTCTCGAAACCTCCCGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTT	720
Qy	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGCGTAAATACGGTTATCCACAGATCA	780
Db	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAAGGCGTAAATACGGTTATCCACAGATCA	780
Qy	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCGTAAC	840
Db	781	GGGGATAACCGAGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGCCGTAAC	840
Qy	841	AAGCCCGGTTCTGGCGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAAT	900
Db	841	AAGCCCGGTTCTGGCGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCGTTCCC	960
Db	901	CGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACACAGGCGTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTCGCTCTCTGTCCGACCCCTGCGGTACCGGATACCTGTC	1020
Db	961	CCTGGAAGCTCCCTCGTCGCTCTCTGTCCGACCCCTGCGGTACCGGATACCTGTC	1020
Qy	1021	GCCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT	1080
Db	1021	GCCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGAGGTATCTCAGT	1080
Qy	1081	TCGGGTAGGTCGTTTCGCTCAAGCTGGGCTGTGCAAGAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCGGGTAGGTCGTTTCGCTCAAGCTGGGCTGTGCAAGAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGCTTATCG	1200
Db	1141	CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGCTTATCG	1200
Qy	1201	CCACTGGCAGCGCTTCTACCAATAATCCCGGATAAACCCAGCGAAACATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGCGCTTCTACCAATAATCCCGGATAAACCCAGCGAAACATTTGAGGTGAT	1260
Qy	1261	AGGTAAGATTATCCGAGGTATGAACAGGAATTTGGACCTTTTACAGATTTACTCTATGA	1320
Db	1261	AGGTAAGATTATCCGAGGTATGAACAGGAATTTGGACCTTTTACAGATTTACTCTATGA	1320
Qy	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Db	1321	AGCGCCATATTTAAAAAGCTACCAAGACGAAAGAGGATGAAGAGGATGAGGAGGAGATTG	1380
Qy	1381	CTTTGAATATATTGACAAATCTGTATAGATTAATCATCTTTTATATAGAGATATCGCG	1440
Db	1381	CTTTGAATATATTGACAAATCTGTATAGATTAATCATCTTTTATATAGAGATATCGCG	1440

Qy	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGGCGACGCCGTATTCAATATATCTATAGAAT	1500
Db	1441	TATGTAAGGATTTTCAGGGGCAAGGCATAGGCGACGCCGTATTCAATATATCTATAGAAT	1500
Qy	1501	GGGCAAGCATAAAACTTGCATGGACTAATGCTTGAAACCCAGGACAATAACCTTTATAG	1560
Db	1501	GGGCAAGCATAAAACTTGCATGGACTAATGCTTGAAACCCAGGACAATAACCTTTATAG	1560
Qy	1561	CTTGTAATAATCTACCAAAAATTTGGTGTTCAAAATCCGCTCCGTCGATCTATGTTATACG	1620
Db	1561	CTTGTAATAATCTACCAAAAATTTGGTGTTCAAAATCCGCTCCGTCGATCTATGTTATACG	1620
Qy	1621	CCAACTTTGAAAAACAACCTTGAAAAAGCTGTCTTCTGCTAATTTAAGGTTTTCAGATGCCAA	1680
Db	1621	CCAACTTTGAAAAACAACCTTGAAAAAGCTGTCTTCTGCTAATTTAAGGTTTTCAGATGCCAA	1680
Qy	1681	GGAAACAGTGAATTTGGAGTTTCGCTCTGTTTATTAATTTAGCTTCTTTGGGCTATCTTTAAATACT	1740
Db	1681	GGAAACAGTGAATTTGGAGTTTCGCTCTGTTTATTAATTTAGCTTCTTTGGGCTATCTTTAAATACT	1740
Qy	1741	GTAGAAAAGAGGAAGGAATAATAAATGGCTAAAAATGAGAAATACACCGGAAATTGAAAAA	1800
Db	1741	GTAGAAAAGAGGAAGGAATAATAAATGGCTAAAAATGAGAAATACACCGGAAATTGAAAAA	1800
Qy	1801	ACTGATCGAAAAATACCGCTCGCTGCGTAAAGATACGGAAGGAATGTCCTCTGCTAAGGTATA	1860
Db	1801	ACTGATCGAAAAATACCGCTCGCTGCGTAAAGATACGGAAGGAATGTCCTCTGCTAAGGTATA	1860
Qy	1861	TAAGCTTGGTGGGAGAAAAATGAAAAACCTATAATTTAAAAATGCAGGACGCGGTATAAAGG	1920
Db	1861	TAAGCTTGGTGGGAGAAAAATGAAAAACCTATAATTTAAAAATGCAGGACGCGGTATAAAGG	1920
Qy	1921	GACCACCTATGATGTGGAAACGGAAAAAGACATGATGCTTATGGCTGGAGAAAGCTGCC	1980
Db	1921	GACCACCTATGATGTGGAAACGGAAAAAGACATGATGCTTATGGCTGGAGAAAGCTGCC	1980
Qy	1981	TGTTTCCAAAGGTCCTGCACCTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATAGTGTA	2040
Db	1981	TGTTTCCAAAGGTCCTGCACCTTTGAAACGGCATGATGCTGGAGCAATCTGCTCATAGTGTA	2040
Qy	2041	GGCGGATGGGTCCTTTGCTCGAAAGATATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Db	2041	GGCGGATGGGTCCTTTGCTCGAAAGATATGAAGATGAACAAAGCCCTGAAAAGATTAT	2100
Qy	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTTA	2160
Db	2101	CGAGCTGTATGCGGAGTGCAATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTTA	2160
Qy	2161	TACGAATAGCTTATAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Db	2161	TACGAATAGCTTATAGACAGCCGCTTAGCCGAATTTGGATTACTTACTGAATAACGATCTGGC	2220
Qy	2221	CGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA	2280
Db	2221	CGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTA	2280
Qy	2281	TGATTTTTTAAAGACCGAAAGCCCGAGAGGAACCTTGCTTTTCCACGCGACCTGGG	2340
Db	2281	TGATTTTTTAAAGACCGAAAGCCCGAGAGGAACCTTGCTTTTCCACGCGACCTGGG	2340
Qy	2341	AGACAGCAACATCTTTGTCGAAAGATGCCAAAGTAAGTGGCTTTTATTTGATCTTTGGGAGAAG	2400
Db	2341	AGACAGCAACATCTTTGTCGAAAGATGCCAAAGTAAGTGGCTTTTATTTGATCTTTGGGAGAAG	2400
Qy	2401	CGGACGGCGCGGAACAAGTGATGACATTTGCTTCTGCGTCCGTCGATCAGGAGGAGTAT	2460
Db	2401	CGGACGGCGCGGAACAAGTGATGACATTTGCTTCTGCGTCCGTCGATCAGGAGGAGTAT	2460
Qy	2461	CGGGAGAACAGTATGTCGAGCTATTTTTTTTGACTTACTCGGGGATCAAGCCTGATTCGGGA	2520
Db	2461	CGGGAGAACAGTATGTCGAGCTATTTTTTTTGACTTACTCGGGGATCAAGCCTGATTCGGGA	2520
Qy	2521	GAAAAATAAAATATTTATTTTTTACTTGGATGAATTTGTTTTAGTACTAGATGTGCGCGCAACG	2580







CURRENT APPLICATION NUMBER: US/09/845,064	
CURRENT FILING DATE: 2001-04-27	
NUMBER OF SEQ ID NOS: 57	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 9	
LENGTH: 6767	
TYPE: DNA	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Description of Artificial Sequence: Plasmid	
OTHER INFORMATION: pmrt1176	
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NAME/KEY: rep origin	
LOCATION: (1)..(654)	
OTHER INFORMATION: Origin of replication ori RK2	
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NAME/KEY: rep origin	
LOCATION: (655)..(1263)	
OTHER INFORMATION: Origin of replication ori ColEI	
FEATURE:	
NAME/KEY: gene	
LOCATION: (1264)..(2603)	
OTHER INFORMATION: NPT III gene coding for neomycin	
OTHER INFORMATION: phosphotransferase and kanamycin resistance	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (2604)..(4098)	
OTHER INFORMATION: trfA locus from pRK2 coding for two proteins, p285	
OTHER INFORMATION: and p382, enabling the increase in the replication	
OTHER INFORMATION: rate	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (4106)..(4271)	
OTHER INFORMATION: T-DNA left border	
FEATURE:	
NAME/KEY: terminator	
LOCATION: (4272)..(4559)	
OTHER INFORMATION: No. US20030175976Alaline synthetase terminator	
FEATURE:	
NAME/KEY: gene	
LOCATION: (4560)..(5556)	
OTHER INFORMATION: Wild type NPT II gene coding for neomycin	
OTHER INFORMATION: transferase and kanamycin resistance	
FEATURE:	
NAME/KEY: promoter	
LOCATION: (5557)..(5771)	
OTHER INFORMATION: No. US20030175976Alaline synthetase promoter	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (5771)..(5830)	
OTHER INFORMATION: MCS multiple cloning site	
FEATURE:	
NAME/KEY: polyA signal	
LOCATION: (5830)..(6560)	
OTHER INFORMATION: Poly A from 35S ribosome	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (6560)..(6587)	
OTHER INFORMATION: MCS multiple cloning site	
FEATURE:	
NAME/KEY: misc feature	
LOCATION: (6587)..(6760)	
OTHER INFORMATION: T-DNA right border	
US-09-845-064-9	
Query Match	
Best Local Similarity 94.3%; Score 4531.4; DB 10; Length 6767;	
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CCGGGCTGGTTGCCCTCGCGCTGGCGCGCGCTATGGCCCTGCAAAACGCGCCAG 60
Db	1 CCGGGCTGGTTGCCCTCGCGCTGGCGCGCGCTATGGCCCTGCAAAACGCGCCAG 60

Qy	61	AAACGCGCTGAAGCGCTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCGG 120
Db	61	AAACGCGCTGAAGCGCTGTGCGAGACACCGCGCGCGCGCGCTTGTGGATACCTCGCGG 120
Qy	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Db	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
Qy	181	CGGCGCGCGCTTGACAGATGAGGGCGGAGCTCGATTTCGGCGCGGCGAGCTGAGCTGGC 240
Db	181	CGGCGCGCGCTTGACAGATGAGGGCGGAGCTCGATTTCGGCGCGGCGAGCTGAGCTGGC 240
Qy	241	CAGCCTCGCAAAATCGCGGAAACGCGCTGATTTTACCGGAGTTTCCACACAGATGATGGGA 300
Db	241	CAGCCTCGCAAAATCGCGGAAACGCGCTGATTTTACCGGAGTTTCCACACAGATGATGGGA 300
Qy	301	CAAGCTTGGGGATAAGTGCCTCGGTATTGACACTTTGAGGGGCGGAGCTACTTGACAGAT 360
Db	301	CAAGCTTGGGGATAAGTGCCTCGGTATTGACACTTTGAGGGGCGGAGCTACTTGACAGAT 360
Qy	361	GAGGGCGGATCCTTGACACTTTGAGGGCGGAGTGTGACAGATGAGGGGCGGACCTAT 420
Db	361	GAGGGCGGATCCTTGACACTTTGAGGGCGGAGTGTGACAGATGAGGGGCGGACCTAT 420
Qy	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGCAAGGGTTTCGCGCCGT 480
Db	421	TGACATTTGAGGGGCTGTCCACAGGCGAGAAATCCAGCATTTTGCAAGGGTTTCGCGCCGT 480
Qy	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540
Db	481	TTTTTCGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTTG 540
Qy	541	TTTTTAAACGAGGCTCGCGCTGTGCGCGTACCGCGGCGGAGGGGGTTCGCCCCC 600
Db	541	TTTTTAAACGAGGCTCGCGCTGTGCGCGTACCGCGGCGGAGGGGGTTCGCCCCC 600
Qy	601	CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAATATCCGCACAGATGCGTAAGAGA 660
Db	601	CTTCTCGAAACCTCCCGGAAAGGTATGCGGTGTGAATATCCGCACAGATGCGTAAGAGA 660
Qy	661	AAATACCGCATCAGGCGCTTTCGCGTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720
Db	661	AAATACCGCATCAGGCGCTTTCGCGTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720
Qy	721	CGGCTGGGCGGAGCGGTATCAGCTCACTCAAGGGCGGTAATACGGTTATCCACAGATCA 780
Db	721	CGGCTGGGCGGAGCGGTATCAGCTCACTCAAGGGCGGTAATACGGTTATCCACAGATCA 780
Qy	781	GGGGATAACGCGAGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCGTAAA 840
Db	781	GGGGATAACGCGAGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCGTAAA 840
Qy	841	AAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCGCTTACGAGCATCAAAAAT 900
Db	841	AAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCCGCTTACGAGCATCAAAAAT 900
Qy	901	CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGGGGTTTCCC 960
Db	901	CGAGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGGGGTTTCCC 960
Qy	961	CTTGGAAAGCTCCCTCGTGGCTCTCTGTTTCGACCCCTGCGGTTACCGGATACCTGTCC 1020
Db	961	CTTGGAAAGCTCCCTCGTGGCTCTCTGTTTCGACCCCTGCGGTTACCGGATACCTGTCC 1020
Qy	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGTTTCTCATAGCTCAAGCTGTAGTATCTCAGT 1080
Db	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGTTTCTCATAGCTCAAGCTGTAGTATCTCAGT 1080
Qy	1081	TCGGTGTAGTTCGTTTCGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCGAC 1140
Db	1081	TCGGTGTAGTTCGTTTCGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCGAC 1140
Qy	1141	CGCTGGCGCTTATCCCGGTAACATATCGTCTTGTAGTCCAAACCCCGTAAGACACGACTTATCG 1200

Db 1141 |||||CGTGGCCCTATCCGGTAATCTCGTCTTGGTCCAAACCCGGTAAAGACACGACTTATCG 1200  
Qy 1201 CCACTGGCAGCAGCTTCTACCAATAATCCCGCATAAACCCAGCGAACCAATTTGAGGTGAT 1260  
Db 1201 CCACTGGCAGCAGCTTCTACCAATAATCCCGCATAAACCCAGCGAACCAATTTGAGGTGAT 1260  
Qy 1261 AGGTAAAGATTATACCGAGGTATGAAAACGAGAAATTGACACTTTACAGAAATTTACTCTATGA 1320  
Db 1261 AGGTAAAGATTATACCGAGGTATGAAAACGAGAAATTGACACTTTACAGAAATTTACTCTATGA 1320  
Qy 1321 AGCGCCATATTTAAAGCTTACCAAGCAGAAAGAGGATGAAGAGATGAGAGGACAGATTG 1380  
Db 1321 AGCGCCATATTTAAAGCTTACCAAGCAGAAAGAGGATGAAGAGATGAGAGGACAGATTG 1380  
Qy 1381 CTTTGAATATATTGACAAATCTGATAAGATAATACATCTTTTATATAGAAGATATCGCCG 1440  
Db 1381 CTTTGAATATATTGACAAATCTGATAAGATAATACATCTTTTATATAGAAGATATCGCCG 1440  
Qy 1441 TATGTAAGGATTTACGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAGGATTTACGGGGCAAGGCATAGGCAGCGCTTATCAATATATCTATAGAAT 1500  
Qy 1501 GGGCAAGCATAAACCTTCATGGACTAATGCTTGNAAACCCAGGACAATAACCTTATAG 1560  
Db 1501 GGGCAAGCATAAACCTTCATGGACTAATGCTTGNAAACCCAGGACAATAACCTTATAG 1560  
Qy 1561 CTTGTAATTTACCAAAATTTGGTTTCAAAATCGCTCCGTCGATACATGCTTATACG 1620  
Db 1561 CTTGTAATTTACCAAAATTTGGTTTCAAAATCGCTCCGTCGATACATGCTTATACG 1620  
Qy 1621 CCAACTTTGAAAAACACTTTTGAAGAGCTGTTTTCTGGTATTTAAGTTTTAGAATGCAA 1680  
Db 1621 CCAACTTTGAAAAACACTTTTGAAGAGCTGTTTTCTGGTATTTAAGTTTTAGAATGCAA 1680  
Qy 1681 GGAACAGTGAATTTGGAGTTTCGTGTTATAATTAATAGCTTCTGGGATATCTTTAAATACT 1740  
Db 1681 GGAACAGTGAATTTGGAGTTTCGTGTTATAATTAATAGCTTCTGGGATATCTTTAAATACT 1740  
Qy 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTAAATGAGAAATATACCCGGAATTTGAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAATGGCTAAATGAGAAATATACCCGGAATTTGAAAA 1800  
Qy 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
Qy 1861 TAAGCTGGTGGAGAAAAATGAAAACCTATATTTTAAATAAGACGGAAGCGGTATAAAG 1920  
Db 1861 TAAGCTGGTGGAGAAAAATGAAAACCTATATTTTAAATAAGACGGAAGCGGTATAAAG 1920  
Qy 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTGGAAGGAAGCTGCC 1980  
Db 1921 GACCACCTATGATGTGAAACGGGAAAGGACATGCTATGCTGGAAGGAAGCTGCC 1980  
Qy 1981 TGTTCAAAAGGTCCTGCACCTTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCAAAAGGTCCTGCACCTTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
Qy 2041 GGCCGATGGCGTCTTGTTCGGAAGATGAAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Db 2041 GGCCGATGGCGTCTTGTTCGGAAGATGAAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
Qy 2101 CGAGCTGTATGCGGAGTGCAATCAGGCTTTTCACTCCATCGACATATCGGATGTCCTTA 2160  
Db 2101 CGAGCTGTATGCGGAGTGCAATCAGGCTTTTCACTCCATCGACATATCGGATGTCCTTA 2160  
Qy 2161 TACGAATAGCTTACAGCGCGCTTAGCCGAATTTGGATTACTTACTGAATAACCATCTGGC 2220  
Db 2161 TACGAATAGCTTACAGCGCGCTTAGCCGAATTTGGATTACTTACTGAATAACCATCTGGC 2220  
Qy 2221 CGATGTGGATTGCGAAACCTGGGAAGAAGACACTCCATTTTAAAGATCCGCGGAGCTGTA 2280

Db 2221 CGATGTGGATTGCGAAAACTGGGAAGAAGACACTCCATTTAAAGATCCGCGGAGCTGTA 2280  
Qy 2281 TGATTTTTTAAAGACGGAAGAGCCCGAAGAGAACTTGTCTTTTCCACGGGACCTGGG 2340  
Db 2281 TGATTTTTTAAAGACGGAAGAGCCCGAAGAGAACTTGTCTTTTCCACGGGACCTGGG 2340  
Qy 2341 AGACAGCAACATCTTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTTGATCTTGGGAAG 2400  
Db 2341 AGACAGCAACATCTTTTGTGAAAGATGGCAAAAGTAAGTGGCTTTATTTGATCTTGGGAAG 2400  
Qy 2401 CGGCGGGCGGACAGTGTGATGACATTTGCTTCTGCGTCCGTCGATCAGGGAGGATAT 2460  
Db 2401 CGGCGGGCGGACAGTGTGATGACATTTGCTTCTGCGTCCGTCGATCAGGGAGGATAT 2460  
Qy 2461 CGGGAAGAACAGTATGTCAGACTATTTTGTGACTTACTTGGGATCAAGCCTGATTTGGGA 2520  
Db 2461 CGGGAAGAACAGTATGTCAGACTATTTTGTGACTTACTTGGGATCAAGCCTGATTTGGGA 2520  
Qy 2521 GAAAATAAAATATATATTTTACTGATGAAATTTGTTTTAGTACCTAGATGTGGCGAACG 2580  
Db 2521 GAAAATAAAATATATATTTTACTGATGAAATTTGTTTTAGTACCTAGATGTGGCGAACG 2580  
Qy 2581 ATGCCGGCACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG 2640  
Db 2581 ATGCCGGCACAGCAGGAGCGCACCGACTTCTTCCGCATCAAGTGTTTTGGCTCTCAGG 2640  
Qy 2641 CCGAGGCCCAACGGCAAGTATTTTGGGCAAGGGTCTGCTGATTTTCGTGACAGGCAAGATTC 2700  
Db 2641 CCGAGGCCCAACGGCAAGTATTTTGGGCAAGGGTCTGCTGATTTTCGTGACAGGCAAGATTC 2700  
Qy 2701 GGAATACCAAGTACGGAAGAGCAGCGCTCTACCGGACCGACTTTCATTTGCCGATA 2760  
Db 2701 GGAATACCAAGTACGGAAGAGCAGCGCTCTACCGGACCGACTTTCATTTGCCGATA 2760  
Qy 2761 AGTGTGATTTCTGACACCAAGGACACAGGCGGGTCAATCAGGAATTAAGGCAATTG 2820  
Db 2761 AGTGTGATTTCTGGAACCAAGGACACAGGCGGGTCAATCAGGAATTAAGGCAATTG 2820  
Qy 2821 CCGCGCGTGAAGTGGGGGCAATCCCGAAGGAGGGTGAATGAATCGGAGCTTTGACCGGA 2880  
Db 2821 CCGCGCGTGAAGTGGGGGCAATCCCGAAGGAGGGTGAATGAATCGGAGCTTTGACCGGA 2880  
Qy 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCCGCAGGATGCCAAACCATCG 2940  
Db 2881 AGGCATACAGGCAAGAACTGATCGACGCGGGGTTTTCCCGCAGGATGCCAAACCATCG 2940  
Qy 2941 CAAAGCGACCGCTCATGCTGCGCCCGCGGAAACCTTCCAGTCCGCTCGATGGTCC 3000  
Db 2941 CAAAGCGACCGCTCATGCTGCGCCCGCGGAAACCTTCCAGTCCGCTCGATGGTCC 3000  
Qy 3001 AGCAAGCTACGCGCAAGATCGAGCGGACAGCGTGCACCTGGCTCCCTCCCTGCCCTGCCG 3060  
Db 3001 AGCAAGCTACGCGCAAGATCGAGCGGACAGCGTGCACCTGGCTCCCTCCCTGCCCTGCCG 3060  
Qy 3061 CGCCATCGGCCCGCGTGGAGCGTTCCGCTGCTCTCGAACAGGAGCGGAGGTTTGGCGGA 3120  
Db 3061 CGCCATCGGCCCGCGTGGAGCGTTCCGCTGCTCTCGAACAGGAGCGGAGGTTTGGCGGA 3120  
Qy 3121 AGTCGATGACCATGACACGCGGAGAACTATGACGACCAAGAGCGGAAAAACCGCCGGCG 3180  
Db 3121 AGTCGATGACCATGACACGCGGAGAACTATGACGACCAAGAGCGGAAAAACCGCCGGCG 3180  
Qy 3181 AGGACTGGCAAAACAGGTACAGGAGGCGCAAGCAGCGCGCTTGTCTGAAACACACGAAGC 3240  
Db 3181 AGGACTGGCAAAACAGGTACAGGAGGCGCAAGCAGCGCGCTTGTCTGAAACACACGAAGC 3240  
Qy 3241 AGCAGATCAAGGAAATGACGCTTCTTGTTCGATATTTGCGCGCTGGCGCGGACAGATGC 3300  
Db 3241 AGCAGATCAAGGAAATGACGCTTCTTGTTCGATATTTGCGCGCTGGCGCGGACAGATGC 3300  
Qy 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCTCTGTTTCAACACGCGGCAACAGAAAATCC 3360  
Db 3301 GAGCGATGCCAAACGACACGCGCGCTCTGCTCTGTTTCAACACGCGGCAACAGAAAATCC 3360

QY 3361 CGCGCGAGCGCTGCRAAAACAAGGTCAATTTTCCACGTCACAAAGGACGTGAAGATCACCT 3420  
Db 3361 CGCGCGAGCGCTGCRAAAACAAGGTCAATTTTCCACGTCACAAAGGACGTGAAGATCACCT 3420  
QY 3421 ACACCGCGCTCGAGCTCGCGGCGCGACGATGACGAACCTGGTGTGGCAGCAGGTGTGGAGT 3480  
Db 3421 ACACCGCGCTCGAGCTCGCGGCGCGACGATGACGAACCTGGTGTGGCAGCAGGTGTGGAGT 3480  
QY 3481 ACGCGAAGCGCACCCCTATCGCGGAGCGCGATTCACCTTTCACGTTCTACGAGCTTTGCCAGG 3540  
Db 3481 ACGCGAAGCGCACCCCTATCGCGGAGCGCGATTCACCTTTCACGTTCTACGAGCTTTGCCAGG 3540  
QY 3541 ACCTGGCTGGTCGATCAATGGCCGGTATTACGAGGCGGAGGATGCTGTCCGCC 3600  
Db 3541 ACCTGGCTGGTCGATCAATGGCCGGTATTACGAGGCGGAGGATGCTGTCCGCC 3600  
QY 3601 TACAGGCGACGGGATGGGCTTCACGTCGACCGCGTGGGCGACCTGGAATCGGTGTGCG 3660  
Db 3601 TACAGGCGACGGGATGGGCTTCACGTCGACCGCGTGGGCGACCTGGAATCGGTGTGCG 3660  
QY 3661 TGCTGCAACCGCTTCGCGTCTCTGACCGTGGCAAGAAAACGTCCCGTTCAGGTCCTGA 3720  
Db 3661 TGCTGCAACCGCTTCGCGTCTCTGACCGTGGCAAGAAAACGTCCCGTTCAGGTCCTGA 3720  
QY 3721 TCGACGAGGAATCGTCTGCTGTCTGCTGGCGACCACTACAGAAATTCATATGGGAGA 3780  
Db 3721 TCGACGAGGAATCGTCTGCTGTCTGCTGGCGACCACTACAGAAATTCATATGGGAGA 3780  
QY 3781 AGTACCCCAAGCTGTCTCCCGACCGCCGACGGATGTTTCGACTATTTTCAGCTCGCACCGGG 3840  
Db 3781 AGTACCCCAAGCTGTCTCCCGACCGCCGACGGATGTTTCGACTATTTTCAGCTCGCACCGGG 3840  
QY 3841 AGCGGTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGCG 3900  
Db 3841 AGCGGTACCGCTCAAGCTGGAACCTTCCGCTCATGTGCGGATCGGATTCACCCCGCG 3900  
QY 3901 TGAAGAGTCGCGGACGAGTGGCGAAGCCTCGAAGAGTTGCGAGGCGAGCGGCTGG 3960  
Db 3901 TGAAGAGTCGCGGACGAGTGGCGAAGCCTCGAAGAGTTGCGAGGCGAGCGGCTGG 3960  
QY 3961 TGAACAACCGCTGGGTCAATGATGACCTGGTGCATTGCAACCGTACGGCTTGTGGGGT 4020  
Db 3961 TGAACAACCGCTGGGTCAATGATGACCTGGTGCATTGCAACCGTACGGCTTGTGGGGT 4020  
QY 4021 CAGTTCCGGCTGGGGTTACAGCAGCAGCGCTTTCCTAGGTTGACGTCCT 4080  
Db 4021 CAGTTCCGGCTGGGGTTACAGCAGCAGCGCTTTCCTAGGTTGACGTCCT 4080  
QY 4081 CTGATGGGCTGCCTGATCGAGTGGTATTTGTCGCGAGCTGCCGTCGGGAGCTGTT 4140  
Db 4081 CTGATGGGCTGCCTGATCGAGTGGTATTTGTCGCGAGCTGCCGTCGGGAGCTGTT 4140  
QY 4141 GGCTGGCTGGTGGCAGGATATATTGGTGTAAACAAATTTGACCTTAGACAACTTAATA 4200  
Db 4141 GGCTGGCTGGTGGCAGGATATATTGGTGTAAACAAATTTGACCTTAGACAACTTAATA 4200  
QY 4201 ACACATTCGCGACGTTTTTAATGTACTGGGCTATCCCCGGGGGATATCATAGGCCCG 4260  
Db 4201 ACACATTCGCGACGTTTTTAATGTACTGGGCTATCCCCGGGGGATATCATAGGCCCG 4260  
QY 4261 ATCTAGTAACATATGACCGCGCGATATTTATCTAGTTTGGCGCTATATTTTG 4320  
Db 4261 ATCTAGTAACATATGACCGCGCGCGATATTTATCTAGTTTGGCGCTATATTTTG 4320  
QY 4321 TTTTCTATCGGTAATAAATGATAATTTGCGGACTCTAATCATAAAAACCATCTCAT 4380  
Db 4321 TTTTCTATCGGTAATAAATGATAATTTGCGGACTCTAATCATAAAAACCATCTCAT 4380  
QY 4381 AATAACGTCATGCAATTCATGTTAATTTATATACGCTTAAGTAATTTCAACAGAAATAT 4440  
Db 4381 AATAACGTCATGCAATTCATGTTAATTTATATACGCTTAAGTAATTTCAACAGAAATAT 4440

QY 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTTAAGAACTTTATTGCCAAATG 4500  
Db 4441 ATGATAATCATCGCAAGACCGCAACAGGATTCATCTTTAAGAACTTTATTGCCAAATG 4500  
QY 4501 TTTGAACGATCGTTCTGTCGAGCTATGGGCCGA 4533  
Db 4501 TTTGAACGATCGTTCTGTCGAGCTATGGGCCGA 4533  
RESULT 12  
US-09-845-064-13  
; Sequence 13, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 6865  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pMRT1195  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:  
; NAME/KEY: rep origin  
; LOCATION: (655)..(1263)  
; OTHER INFORMATION: Origin of replication ori ColEI  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1264)..(2603)  
; OTHER INFORMATION: NPT III gene coding for neomycin  
; OTHER INFORMATION: phosphotransferase and kanamycin resistance  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2604)..(4098)  
; OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285  
; OTHER INFORMATION: and P382, enabling the increase in the replication  
; OTHER INFORMATION: rate  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4106)..(4271)  
; OTHER INFORMATION: T-DNA left border  
; FEATURE:  
; NAME/KEY: terminator  
; LOCATION: (4272)..(4559)  
; OTHER INFORMATION: No. US20030175976Ala1line synthetase terminator  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (4575)..(5150)  
; OTHER INFORMATION: Bar gene coding for phosphinotricin  
; OTHER INFORMATION: acetyltransferase and glufosinate resistance  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (5174)..(5685)  
; OTHER INFORMATION: Rice Actin Intron  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (5686)..(6626)  
; OTHER INFORMATION: Rice Actin promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (6626)..(6685)

; OTHER INFORMATION: MCS multiple cloning site

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (6685)..(6858)

; OTHER INFORMATION: T-DNA right border

US-09-845-064-13

Query Match 94.3%; Score 4531.4; DB 10; Length 6865;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	CCGGCTGGTTCCTCGCGCTGGGCTGGGCTGGGCGGCTGATGGCCCTGCAAAAGCGCCAG	60
Db	1	CCGGCTGGTTCCTCGCGCTGGGCTGGGCTGGGCGGCTGATGGCCCTGCAAAAGCGCCAG	60
Qy	61	AAACCGCTCGAAGCGGTGTCAGACACACCGCGCGCGGTGTTGGATACCTCGCGG	120
Db	61	AAACCGCTCGAAGCGGTGTCAGACACACCGCGCGCGGTGTTGGATACCTCGCGG	120
Qy	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC	180
Db	121	AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCGGACTCAC	180
Qy	181	CCGGCGCGGCTTGACAGATGAGGGCGGACGTTGACACTTGGCGCGGACGTTGAGCTGGC	240
Db	181	CCGGCGCGGCTTGACAGATGAGGGCGGACGTTGACACTTGGCGCGGACGTTGAGCTGGC	240
Qy	241	CAGCTCGCAAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGA	300
Db	241	CAGCTCGCAAAATCGGCGAAACGCTGATTTTACGCGAGTTTCCCAACAGATGATGGA	300
Qy	301	CAAGCTTGGGGATGAAGTGCCTCGGTATTTGACACTTGAAGGGCGGACTACTGACAGAT	360
Db	301	CAAGCTTGGGGATGAAGTGCCTCGGTATTTGACACTTGAAGGGCGGACTACTGACAGAT	360
Qy	361	GAGGGCGGATCTTGACACTTTGAGGGCAGAGTGTGACAGATGAGGGCGGACCTAT	420
Db	361	GAGGGCGGATCTTGACACTTTGAGGGCAGAGTGTGACAGATGAGGGCGGACCTAT	420
Qy	421	TGACATTTGAGGGCTGTCCACAGGCAAGAAATCCAGCATTTGCAAGGGTTTCGCGCGT	480
Db	421	TGACATTTGAGGGCTGTCCACAGGCAAGAAATCCAGCATTTGCAAGGGTTTCGCGCGT	480
Qy	481	TTTTTGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Db	481	TTTTTGGCCACCGCTAACCTGTCTTTTAACTGCTTTTAAACCAATATTTATAAACCCTG	540
Qy	541	TTTTTAAACAGGGTGGCCCTGTGCGGTGAACCGGCAACCGGAGGGGGTGCCTCCC	600
Db	541	TTTTTAAACAGGGTGGCCCTGTGCGGTGAACCGGCAACCGGAGGGGGTGCCTCCC	600
Qy	601	CTTCTCGAACCCCTCCGGAAGGTATCGGTGTGAAATACCGACAGATCGTAAAGAGA	660
Db	601	CTTCTCGAACCCCTCCGGAAGGTATCGGTGTGAAATACCGACAGATCGTAAAGAGA	660
Qy	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTCACTCGCTCGCTCGGCTGTT	720
Db	661	AAATACCGCATCAGGCGCTCTTCGCTTCTCGCTCACTCACTCGCTCGCTCGGCTGTT	720
Qy	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACCGGTATTCACAGAAATCA	780
Db	721	CGGCTCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACCGGTATTCACAGAAATCA	780
Qy	781	GGGATTAACCCAGGAAAGATCATGTGAGCAAAAGGCGCAAAAGGCGGAGAAACCGTAAA	840
Db	781	GGGATTAACCCAGGAAAGATCATGTGAGCAAAAGGCGCAAAAGGCGGAGAAACCGTAAA	840
Qy	841	AAGCGCGCTGTGCTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Db	841	AAGCGCGCTGTGCTGGCGTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAAT	900
Qy	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGGTTTCCC	960
Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGGTTTCCC	960

Db	901	CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGGTTTCCC	960
Qy	961	CCTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Db	961	CCTGGAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCC	1020
Qy	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Db	1021	GCCTTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT	1080
Qy	1081	TCGGTGTAGGTCTGTTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC	1140
Db	1081	TCGGTGTAGGTCTGTTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGAC	1140
Qy	1141	CGCTGCGCCTTATCCGCTAACCTATCTCTTGGAGTCAACCCGCTTAAGACACGACTTATCG	1200
Db	1141	CGCTGCGCCTTATCCGCTAACCTATCTCTTGGAGTCAACCCGCTTAAGACACGACTTATCG	1200
Qy	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCGAGCGAACCATTTGAGGTGAT	1260
Db	1201	CCACTGGCAGCAGCTTCTACCAATAATCCGCGATAAACCCGAGCGAACCATTTGAGGTGAT	1260
Qy	1261	AGGTAAGATTAATCCGAGGTATGAAAAAGGAAATTCGACTTTTACAGAAATCTCTATGA	1320
Db	1261	AGGTAAGATTAATCCGAGGTATGAAAAAGGAAATTCGACTTTTACAGAAATCTCTATGA	1320
Qy	1321	AGCGCCATATTTTAAAGCTTACCAAGCAAGAGGATGAAGAGGATGAGGAGGAGGATG	1380
Db	1321	AGCGCCATATTTTAAAGCTTACCAAGCAAGAGGATGAAGAGGATGAGGAGGAGGATG	1380
Qy	1381	CCTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG	1440
Db	1381	CCTTGAATATATTGACAATACTGATAAGATAATACATCTTTTATATAGAGATATCGCCG	1440
Qy	1441	TATGTAAGGATTTTACGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAAT	1500
Db	1441	TATGTAAGGATTTTACGGGGCAAGGCATAGGCGCGCTTATCAATATATCTATAGAAAT	1500
Qy	1501	GGGCAAGGATATAAACTTGCATGGAATAATGCTTGAACCCAGGACAAATACCTATAG	1560
Db	1501	GGGCAAGGATATAAACTTGCATGGAATAATGCTTGAACCCAGGACAAATACCTATAG	1560
Qy	1561	CTTGTAAATTTTACCAAAATTTGCTTCAAAATCGGCTCGCTCGATATCTATATACG	1620
Db	1561	CTTGTAAATTTTACCAAAATTTGCTTCAAAATCGGCTCGCTCGATATCTATATACG	1620
Qy	1621	CCAACTTTGAAAAACAACTTTGAAAAAGCTGTTTCTGTTATTTAAGGTTTGAAGTCAA	1680
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Qy	1801	ACTGATCGAAAAATACCGCTGCGTAAAAAGATACGGAAGGAAATGCTCTGCTAAGGTATA	1860
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Qy	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTTATGGCTGGAAGGAAAGTGGC	1980
Db	1921	GACCACTATGATGTGAAACGGGAAAGGACATGATGCTTATGGCTGGAAGGAAAGTGGC	1980
Qy	1981	TGTTCCAAAGGCTCTGCACTTTTGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGA	2040
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Db	2041		
QY	2101	CGAGCTGTATCGCGAGTGCATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCTTA	2160
Db	2101		
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Db	2161		
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Db	2221		
QY	2281	TGATTTTTTAAAGACGGAAAGCCGAAGGAACTTGTCTTTTCCACGGCAGCTGGG	2340
Db	2281		
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Db	2341		
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Db	2401		
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Db	2461		
QY	2521	GAAATATAATATTTATCTGGATGAATTTGTTTATGTAACCTAGATGTGGCGCAACG	2580
Db	2521		
QY	2581	ATCCCGGCACAGCAGGCGCACCTCTTCCGCATCAAGTGTTTTGGCTCTCAGG	2640
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Db	2641		
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Db	3961		
QY	4021	CAGTTCGGCTGGGGTTACAGCAGCAGCGCTTTTACTGGCATTTCTAGGTTCAGCTCTT	4080
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Db	4201		



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RESULT 14

US-09-845-064-19  
; Sequence 19, Application US/09845064  
; Publication No. US20030175976A1  
; GENERAL INFORMATION:  
; APPLICANT: MERISTEM THERAPEUTICS  
; TITLE OF INVENTION: CLSAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS  
; AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR  
; TITLE OF INVENTION: METHODS OF PRODUCTION  
; FILE REFERENCE: SynVec1  
; CURRENT APPLICATION NUMBER: US/09/845,064  
; CURRENT FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 7503  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid  
; OTHER INFORMATION: pMR1205  
; FEATURE:  
; NAME/KEY: rep\_origin  
; LOCATION: (1)..(654)  
; OTHER INFORMATION: Origin of replication ori RK2  
; FEATURE:

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/ NAME/KEY: gene
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/ OTHER INFORMATION: NPT III gene coding for neomycin
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/ NAME/KEY: misc_feature
/ LOCATION: (2604)..(4098)
/ OTHER INFORMATION: TrfA locus from RK2 coding for two proteins, P285
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/ OTHER INFORMATION: rate
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/ OTHER INFORMATION: Poly A from 35S ribosome
/ FEATURE:
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/ OTHER INFORMATION: MCS multiple cloning site
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (7323)..(7496)
/ OTHER INFORMATION: T-DNA right border
/ US-09-845-064-19
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Query Match          94.3%; Score 4531.4; DB 10; Length 7503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      61  AAACCGCGTGAACCGGTGTCGAGACACCCGCGCGCGCGGTGTGGATACCTCGGG 120

Qy      121  AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCCGACTCAC 180
Db      121  AAAACTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAAGGGCCGACTCAC 180

Qy      181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGGACGCTGGAGCTGGC 240
Db      181  CCGCGCGCGGCTTGACAGATGAGGGCGAGGCTCGATTTCCGCGCGGACGCTGGAGCTGGC 240
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Qy      361  GAGGGCGCGATCCTTTGACACTTGAAGGGCGAGTGTCTCAGAGATGAGGGCGCACCTAT 420
Db      361  GAGGGCGCGATCCTTTGACACTTGAAGGGCGAGTGTCTCAGAGATGAGGGCGCACCTAT 420

Qy      421  TGACATTTGAGGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTCAAGGGTTTCCGGCCGT 480
Db      421  TGACATTTGAGGGGCTGTCCACAGGCAGAAAAATCCAGCATTTTCAAGGGTTTCCGGCCGT 480

Qy      481  TTTTTCGGCACCGCTAACCTGTCTTTTAACCTGCTTTTAAACCAATATTTATAAACCCTTG 540
Db      481  TTTTTCGGCACCGCTAACCTGTCTTTTAAACCTGCTTTTAAACCAATATTTATAAACCCTTG 540

Qy      541  TTTTAAACAGGGCTCGCCCTGTGCGGTGACCGCGCACCGCAAGGGGGTGCCTCCCC 600
Db      541  TTTTAAACAGGGCTCGCCCTGTGCGGTGACCGCGCACCGCAAGGGGGTGCCTCCCC 600

Qy      601  CTTTCTCGAAACCTTCCCGGAAAGGTATCGCGTGTGAAATACCGCACAGATGCGTAAGAGA 660
Db      601  CTTTCTCGAAACCTTCCCGGAAAGGTATGCGGTGTGAAATACCGCACAGATGCGTAAGAGA 660

Qy      661  AAATACCGCATCAGGGCGCTTTCGGTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720
Db      661  AAATACCGCATCAGGGCGCTTTCGGTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTT 720

Qy      721  CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGGGGTAAATACGTTTATCCACAGAAATCA 780
Db      721  CGGCTGGCGGAGCGGTATCAGCTCACTCAAAGGGGTAAATACGTTTATCCACAGAAATCA 780

Qy      781  GGGGATAAAGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 840
Db      781  GGGGATAAAGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAA 840

Qy      841  AAGGCGCGTGTGCTGGGTTTTTCCATAGGCTCGGCCCTCGCCCTCAGCAGCATCAAAAAT 900
Db      841  AAGGCGCGTGTGCTGGGTTTTTCCATAGGCTCGGCCCTCGCCCTCAGCAGCATCAAAAAT 900

Qy      901  CGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACACGAGGCTTTCCC 960
Db      901  CGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACACGAGGCTTTCCC 960

Qy      961  CTTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCTCGCGTTTACCAGATACCTGTCC 1020
Db      961  CTTGGAAGCTCCCTCGTGGCGCTCTCCTGTTCCGACCTCGCGTTTACCAGATACCTGTCC 1020

Qy      1021  GCCTTTCTCCCTTCGGGAACGCTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080
Db      1021  GCCTTTCTCCCTTCGGGAACGCTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGT 1080

Qy      1081  TCGGTGTAGTTCGCTTCGCTCAAGCTGGGTGTGTCACGAAACCCCGCTTCAGCCCGAC 1140
Db      1081  TCGGTGTAGTTCGCTTCGCTCAAGCTGGGTGTGTCACGAAACCCCGCTTCAGCCCGAC 1140

Qy      1141  CGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTGAAGACAGCTTATCG 1200
Db      1141  CGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAAACCCGGTGAAGACAGCTTATCG 1200

Qy      1201  CCACTGCGCAGCGCTTCTACCATATTCGCGATTAACCCAGCGAACCATTTGAGGTGAT 1260
Db      1201  CCACTGCGCAGCGCTTCTACCATATTCGCGATTAACCCAGCGAACCATTTGAGGTGAT 1260

Qy      1261  AGTTAAGATTTATCCGAGGTATGAACAGAAATGGACCTTTACAGAAATTTACTCTATGA 1320
Db      1261  AGTTAAGATTTATCCGAGGTATGAACAGAAATTTGGACCTTTTACAGAAATTTACTCTATGA 1320

Qy      1321  AGCGCCATATTTAAAAAGCTTACCAAGACGAAGAGGATGAAGAGGATGAGGAGGAGGATTTG 1380
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Db 1321 ||||| AGCCCATATTTTAAAGCTTACCAAGCGAAGAGGATGAAGAGATGAGGAGCAGATTG 1380  
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Db 1381 CCTTGAATATATTGACAACTACTGATAGATAATACACTCTTTTATATAGAGATATCGCCG 1440  
QY 1441 TATGTAAAGGATTTTCAGGGGCAAGGCATAGGCGAGCGCTTATCAATATATCTATAGAAT 1500  
Db 1441 TATGTAAAGGATTTTCAGGGGCAAGGCATAGGCGAGCGCTTATCAATATATCTATAGAAT 1500  
QY 1501 GGGCAAGCATATAAACTTCATGAGACTAATGCTTGAACCCAGGACATAAACCCTTATAG 1560  
Db 1501 GGGCAAGCATATAAACTTCATGAGACTAATGCTTGAACCCAGGACATAAACCCTTATAG 1560  
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Db 1561 CTTGTAAATTTCTACCAAAATTTGCTTCAAAATCGSCTCCGTCGATACTATGTTATACG 1620  
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Db 1621 CCAACTTTGAAAAACACTTTGAAAAAGCTGTTTTCTGGTATTTAAAGTTTTAGAAATGCAA 1680  
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Db 1681 GGAACAGTGAATTTGGAGTTTCGCTTGTATATAATTAGCTTCTGGGTATCTTTAAATACT 1740  
QY 1741 GTAGAAAAGAGGAAGAAATAATAATGCTTAAATCGAATATATACCCGAAATGAAAAA 1800  
Db 1741 GTAGAAAAGAGGAAGAAATAATAATGCTTAAATCGAATATATACCCGAAATGAAAAA 1800  
QY 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
Db 1801 ACTGATCGAAAAATACCGCTGCGTAAAGATACGGAAGGAATGCTCTCTGCTAAGGTATA 1860  
QY 1861 TAAAGTGGTGGGAGAAAAAGAAACCTATATTTTAAAAATGACGGAAGCGGTATAAAGG 1920  
Db 1861 TAAAGTGGTGGGAGAAAAAGAAACCTATATTTTAAAAATGACGGAAGCGGTATAAAGG 1920  
QY 1921 GACCACTATGATGTGGAACGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC 1980  
Db 1921 GACCACTATGATGTGGAACGGAAAGGACATGATGCTATGCTGGAAGGAAGCTGCC 1980  
QY 1981 TGTTCAAAGGCTCTGCACATTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
Db 1981 TGTTCAAAGGCTCTGCACATTTGAAACGGCATGATGCTGAGCAATCTGCTCATGAGTGA 2040  
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Db 2041 GGCAGATGGCGTCTTTGCTCGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTAT 2100  
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Db 2101 CGAGCTGTATGGGAGTGCATCAGGCTCTTTTCACTCATCGACATATCGGATTTGCCCTA 2160  
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Db 2161 TACGAATAGCTTACAGACGCGCTTAGCCGAATTTGGATTACTTACTGAATAACCATCTGCC 2220  
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Db 2401 CGGACGGCGGCAAGTGGTATGACATTTGCTTCTGCTCCGTCGATCAGGAGGATAT 2460  
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Db 2461 CGGGGAAGAACAGTATGTGAGCTATTTTTCATCTTACTGGGATCAAGCTCATTTGGGA 2520  
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QY 2641 CCAGAGCCCAACGGCAAGTATTTGGGCAAGGGGTCGCTGATTTCTGTCAGGCGAAGATTC 2700  
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QY 3181 AGGACCTGGCAAAACAGGTCAGCGGCGCAAGCGGCGGTTGCTGAAACACACGAAGC 3240  
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QY 3901 TGAAGAAAGTCGCGACAGAGTCGGCGAAGCTCGGAAGAGTTGCGAGGAGCGGCTGG 3960
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Db 4141 GGCTGGCTGGGAGGATATATTGTTGTTGTAACAAATTCAGCCTTAGACAACTTAATA 4200
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QY 4501 TTTTGAACGATCGTTCGAGCTATGGGCCGA 4533
Db 4501 TTTGAACGATCGTTCGAGCTATGGGCCCAA 4533
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RESULT 15

US-09-845-064-55

; Sequence 55, Application US/09845064

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; Publication No. US20030175976A1
; GENERAL INFORMATION:
; APPLICANT: MERISTEM THERAPEUTICS
; TITLE OF INVENTION: CLEAN SYNTHETIC VECTORS, PLASMIDS, TRANSGENIC PLANTS
; TITLE OF INVENTION: AND PLANT PARTS CONTAINING SAID VECTORS, AND THEIR
; FILE REFERENCE: SynVec1
; CURRENT APPLICATION NUMBER: US/09/845,064
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 8289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMRT1337
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: pMRT1337 was obtained from the insertion, into
; OTHER INFORMATION: pMRT1205, of the gfp gene isolated from
; OTHER INFORMATION: pBINm-gfp5-ER
; US-09-845-064-55
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Query Match          94.3%; Score 4531.4; DB 10; Length 8289;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4532; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1  CCGGGCTGGTTGGCTTCGCCCTGGCGCTGGGCTGGCGGCGCTCTATGGCCCTCAAAACGCGCCAG 60
Db 1  CCGGGCTGGTTGGCTTCGCCCTGGCGCTGGGCTGGCGGCGCTCTATGGCCCTCAAAACGCGCCAG 60

QY 61  AAACGCGCTGAAACCGCTGTGCGAGACACCGCGGCGCGCGCTTGTGGATACCTCGCGG 120
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QY 121 AAACCTTGGCCCTCACTGACAGATGAGGGCGGACGTTGACACTTGAGGGGCGGACTCAC 180
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QY 181 CCGGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTTCGGCCGCGGACGCTGGAGCTGGC 240
Db 181 CCGGCGCGGCTTGACAGATGAGGGCGGACGCTCGATTTTCGGCCGCGGACGCTGGAGCTGGC 240

QY 241 CAGCCTCGCAAAATCGCGGAAACCGCTGATTTTACCGAGTTTCCACAGATGATGGA 300
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QY 301 CAAGCCTGGGGATAAGTGCCTCGGTTATGACACTTGAGGGGCGGACTACTGACAGAT 360
Db 301 CAAGCCTGGGGATAAGTGCCTCGGTTATGACACTTGAGGGGCGGACTACTGACAGAT 360

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QY 421 TGACATTTGAGGGGCTGTCCACAGGAGAAATCCAGCATTTGCAAGGGTTTCGCGCGT 480
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QY 601 CTTCTCGAACCCCTCCCGGAAAGGATGCGGTGTGAAATACCGCACAGATCGGTAAGAGA 660
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Db 1741 GTAGAAAAGAGGAGGAAATAATAAATGGCTAAATAAGAGATATACCCGGAAATTGAAAAA 1800  
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 Db 1861 TAAAGCTGGTGGGAGAAAAATGAAACCTTATATTTAAAAATGACGACACCGCGTATAAAGG 1920  
 Qy 1921 GACCACCTATGATGTCGAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
 Db 1921 GACCACCTATGATGTCGAACGGGAAAGGACATGATGCTATGCTGGAAGGAAAGCTGCC 1980  
 Qy 1981 TGTTCCAAAGGCTCTGCACCTTTTGAAACGGCATGCTGAGCAATCTGCTCATGAGTGA 2040  
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 Qy 2041 GSCCGATGGCGTCTTTTGTCTCGGAAGATGATGAAGATGAAACAAAGCCCTGAAAAGATTAT 2100  
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4501 TTTTGAACGATCGTTCTGTCGAGCTATCGGCCCGA 4533

Search completed: July 20, 2004, 11:37:01  
Job time : 1973 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2004, 11:04:20 ; Search time 11262 Seconds  
(without alignments)  
12740.879 Million cell updates/sec

Title: US-09-845-064-10  
Perfect score: 4805  
Sequence: 1 cggggtggtgcctcgcc.....gagcgcttggagcgctca 4805

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST.\*
- 1: em\_estba.\*
  - 2: em\_esthum.\*
  - 3: em\_estin.\*
  - 4: em\_estnu.\*
  - 5: em\_estov.\*
  - 6: em\_estpl.\*
  - 7: em\_estro.\*
  - 8: em\_htc.\*
  - 9: gb\_est1.\*
  - 10: gb\_est2.\*
  - 11: gb\_htc.\*
  - 12: gb\_est3.\*
  - 13: gb\_est4.\*
  - 14: gb\_est5.\*
  - 15: em\_estfun.\*
  - 16: em\_estom.\*
  - 17: em\_gss\_hum.\*
  - 18: em\_gss\_inv.\*
  - 19: em\_gss\_pln.\*
  - 20: em\_gss\_vrt.\*
  - 21: em\_gss\_fun.\*
  - 22: em\_gss\_mam.\*
  - 23: em\_gss\_mus.\*
  - 24: em\_gss\_pro.\*
  - 25: em\_gss\_rod.\*
  - 26: em\_gss\_pbg.\*
  - 27: em\_gss\_vrl.\*
  - 28: gb\_gss1.\*
  - 29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	11.4	954	9	AL044364
2	546.8	11.4	699	14	CB879625
3	544.2	11.3	582	14	CB872328
4	544.2	11.3	604	14	CB872523

5	544.2	11.3	619	29	CG711606
6	544.2	11.3	656	14	CB858283
7	544.2	11.3	669	13	BQ660152
8	544.2	11.3	677	14	CB865829
9	544.2	11.3	695	13	BQ660140
10	544.2	11.3	700	13	BQ660226
11	544.2	11.3	703	9	AJ281437
12	544.2	11.3	863	14	CF752100
13	544.2	11.3	966	28	BZ570738
14	544.2	11.3	996	29	CG392995
15	544.2	11.3	1089	9	AU081124
16	543.4	11.3	925	14	CB686151
17	543.2	11.3	628	14	CB872076
18	543.2	11.3	680	28	BH235176
19	543.2	11.3	687	9	AU001481
20	542.6	11.3	1073	14	CF269652
21	542.6	11.3	1249	28	BZ572284
22	542	11.3	691	14	CB875232
23	541	11.3	1067	9	AU081137
24	541	11.3	1387	28	BZ577525
25	540.6	11.3	1346	28	BZ572730
26	540	11.2	914	28	BZ569398
27	537.8	11.2	1369	28	BZ579291
28	537.6	11.2	565	14	CB871309
29	536.8	11.2	620	14	CB858957
30	536.6	11.2	593	14	CB858509
31	536.4	11.2	1038	28	BZ549934
32	536.2	11.2	1304	28	BZ576307
33	536	11.2	673	14	CB864014
34	536	11.2	835	28	BZ571572
35	536	11.2	1341	28	BZ576229
36	535.2	11.1	567	29	CG707935
37	535.2	11.1	583	14	CB859700
38	535.2	11.1	663	9	AU001472
39	534.6	11.1	906	29	CG839354
40	533.2	11.1	605	14	CB859681
41	533.2	11.1	621	14	CB872402
42	533.2	11.1	649	14	CB859824
43	533.2	11.1	662	14	CB880413
44	533	11.1	896	28	BZ551301
45	533	11.1	902	28	BZ566804

ALIGNMENTS

RESULT 1	AL044364	954 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	DKFZp434C172.3	434	(synonym: htesa)	Homo sapiens	cdna clone
DEFINITION	DKFZp434C172.3, mRNA sequence.				
ACCESSION	AL044364				
VERSION	AL044364.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 954)				
TITLE	Wiemann, S.				
JOURNAL	EST (Ansoerge, Benes, et al.)				
COMMENT	Unpublished (1999)				
	Contact: MIPS				
	MIPS				
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany				
	This is the 3' sequence of the clone insert				
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;				
	Sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cdna sequencing consortium of the German Genome Project.				
	No r1 sequence available.				



This clone (DKF2p343C172) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

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/clone\_lib="434 (synonym: htes3)"  
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ORIGIN

Query Match 11.4%; Score 547; DB 9; Length 954;  
Best Local Similarity 93.5%; Pred. No. 2e-114;  
Matches 571; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
QY 605 TCGAACCTCCCGAAAGTATGCGGTGTAATACCGCACAGATGCGTTAAGGAGAAAT 664  
DB 161 TCGCGCGAATTGCAAGCTCTGCATTAATGAATCGGCCAACGCGGGAGAGCGGTT 220  
QY 665 ACCGCATCAGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGGTTTCGGC 724  
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QY 725 TCGCGGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAAGGG 784  
DB 281 TCGCGGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAAGGG 340  
QY 785 ATAAACGAGAAAGAACATGTGAGCAAAAGCCAGCAAAAGCGCAGGAAACGTTAAAGG 844  
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QY 845 CCGGTTGCTGGGTTTTTCATAGGCTCGCCCCCTCGAGCATCACAAAATCGAC 904  
DB 401 CCGGTTGCTGGGTTTTTCATAGGCTCGCCCCCTCGAGCATCACAAAATCGAC 460  
QY 905 GCTCAAGTCAGAGGTGGCAAAACCGACAGACTATATAAGTACACAGCGGTTTCCCGCTG 964  
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QY 965 GAAGCTCCCTCGTGCCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCCT 1024  
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QY 1085 TGTAGTTCGTTTCGCTCAAGTGGGCTGTGTGACGAACCCCGCTTCAGCCGACCGCT 1144  
DB 641 TGTAGTTCGTTTCGCTCAAGTGGGCTGTGTGACGAACCCCGCTTCAGCCGACCGCT 700  
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DB 701 GCGCTTTATCGGTAATATCTGTTGAGTCCAAACCGGTAAGACAGACTTATCGCCAC 760  
QY 1205 TGGCAGCAGCC 1215  
DB 761 TGGCAGCAGCC 771

RESULT 2  
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LOCUS  
DEFINITION  
HP03A17w HP Hordeum vulgare subsp. vulgare cDNA clone HP03A17  
3-PRIME, mRNA sequence.  
ACCESSION  
CB879625  
VERSION  
CB879625.1 GI:30081611  
KEYWORDS  
EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Scrophophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 699)  
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.  
EST sequencing and analysis in barley (2002)  
Unpublished (2002)  
Contact: Stein Nils  
Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 699 Std Error: 0.00  
Plate: 3 row: A column: 17  
Seq primer: T7

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 850 bp"

ORIGIN

Query Match 11.4%; Score 546.8; DB 14; Length 699;  
Best Local Similarity 95.4%; Pred. No. 2e-114;  
Matches 563; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
QY 626 TGGGTTGTAATACCGCACAGATGCGTTAAGGAGAAATACCGCATCAGCGCTCTTCCG 685  
DB 38 TGATTAATGAATCCGCCAACGCCGCTGAGGCGGTTTGGTATTTGGCGCTCTTCCG 97  
QY 686 TTTCCTCGCTCACTGACTCGCTCGCTCGGTCGTTCCGGTTCGCGGAGCGGTATCAGCTC 745  
DB 98 TTTCCTCGCTCACTGACTCGCTCGCTCGGTCGTTCCGGTTCGCGGAGCGGTATCAGCTC 157  
QY 746 ACTCAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACCGAGGAAACATGT 805  
DB 158 ACTCAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACCGAGGAAACATGT 217  
QY 806 GAGCAAAAGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGTTGCTGGCGCTTTTCC 865  
DB 218 GAGCAAAAGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGGTTGCTGGCGCTTTTCC 277  
QY 866 ATAGGCTCGCCCCCTCGACGAGCATCACAAAAATCGACGCTCAAGTCAAGTCAAGTGGCGAA 925  
DB 278 ATAGGCTCGCCCCCTCGACGAGCATCACAAAAATCGACGCTCAAGTCAAGTGGCGAA 337  
QY 926 ACCCGACAGACTATAAAGATACCGAGCGTTTCCCTCGGAAGCTCCCTCGGCTCTC 985  
DB 338 ACCCGACAGACTATAAAGATACCGAGCGTTTCCCTCGGAAGCTCCCTCGGCTCTC 397  
QY 986 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTCCGCTTCTTCTCCCTTCGGAAGCGTGG 1045

Db 398 CTGTTCCGACCCCTTACCGGATACCTGTGCCGCTTTCTCCCTTCGCGAAGCGTGG 457  
Qy 1046 CGCTTTCTCATAGCTACCGCTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCAAGC 1105  
Db 458 CGCTTTCTCATAGCTACCGCTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCNAGC 517  
Qy 1106 TGGGCTGTGTGCAGAACCCCGCTTCAGCCCGACCGCTCGGCTTATCCGGTAACATATC 1165  
Db 518 TGGGCTGTGTGCAGAACCCCGCTTCAGCCCGACCGCTCGGCTTATCCGGTAACATATC 577  
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RESULT 3  
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LOCUS CB872328 582 bp mRNA linear EST 03-JUL-2003  
DEFINITION HC07102Y CH Hordeum vulgare cDNA clone HC07102 3-PRIME, mRNA  
sequence.  
CB872328  
VERSION CB872328.1 GI:30074308  
KEYWORDS EST.  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 582)  
AUTHORS Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.  
TITLE Barley ESTs from coleoptile tissue  
JOURNAL Unpublished (2003)  
COMMENT Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
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Site 2: NotI (3-end of cDNA); Due to the cloning system  
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reliable. Average insert size is 1.3 Kb."

Query Match 11.3%; Score 544.2; DB 14; Length 582;  
Best Local Similarity 99.5%; Pred. No. 7.4e-114;  
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 667 CGCATCAGGCGCTTCTCCGCTTCTCGCTCACTCACTCGCTCGGCTCGGCTGCTG 726  
Db 2 CGTATTGGCGCTTCTCCGCTTCTCGCTCACTCACTCGCTCGGCTCGGCTGCTG 61  
Qy 727 CGGGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCAGGGAT 786  
Db 62 CGGCGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCAGGGAT 121

ORIGIN

Query Match 11.3%; Score 544.2; DB 14; Length 582;  
Best Local Similarity 99.5%; Pred. No. 7.4e-114;  
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 667 CGCATCAGGCGCTTCTCCGCTTCTCGCTCACTCACTCGCTCGGCTCGGCTGCTG 726  
Db 2 CGTATTGGCGCTTCTCCGCTTCTCGCTCACTCACTCGCTCGGCTCGGCTGCTG 61  
Qy 727 CGGGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCAGGGAT 786  
Db 62 CGGCGACCGGTATCAGCTCACTCAAGCGGTATACGGTTATCCACAGATCAGGGAT 121

Qy 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGCCAGGAACCGTAAAAAGGCC 846  
Db 122 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGCCAGGAACCGTAAAAAGGCC 181  
Qy 847 GCGTTCTCGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGC 906  
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Qy 907 TCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCCCTGGA 966  
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Qy 967 AGTCCTCTCGTGGCTCTCTCTGTCGACCCCTGCGGCTTACCGGATACCTGTGCGCTTT 1026  
Db 302 AGTCCTCTCGTGGCTCTCTCTGTCGACCCCTGCGGCTTACCGGATACCTGTGCGCTTT 361  
Qy 1027 CTCCTTCGCGAGCGTGGGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTGCGTG 1086  
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Qy 1087 TAGTCTGTTCCGCTCCAAGCTGGGCTGTGTCACGAACCCCGCTTCAGCCCCGACCGCTGC 1146  
Db 422 TAGTCTGTTCCGCTCCAAGCTGGGCTGTGTCACGAACCCCGCTTCAGCCCCGACCGCTGC 481  
Qy 1147 GCCTTATCCGGTAACTATCTCTTGTAGTCCAAACCCCGTAAAGACACGACTTATCGCCTG 1206  
Db 482 GCCTTATCCGGTAACTATCTCTTGTAGTCCAAACCCCGTAAAGACACGACTTATCGCCTG 541  
Qy 1207 GCAGCAGCC 1215  
Db 542 GCAGCAGCC 550

RESULT 4

CB872523  
LOCUS CB872523 604 bp mRNA linear EST 03-JUL-2003  
DEFINITION HC08007Y CH Hordeum vulgare cDNA clone HC08007 3-PRIME, mRNA  
sequence.  
CB872523  
VERSION CB872523.1 GI:30074503  
KEYWORDS EST.  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 604)  
AUTHORS Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and Graner,A.  
TITLE Barley ESTs from coleoptile tissue  
JOURNAL Unpublished (2003)  
COMMENT Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 604 Std Error: 0.00  
Plate: 8 row: G column: 7  
Seq primer: SP6.

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/clone="HC08007"  
/tissue\_type="coleoptile"  
/dev\_stage="coleoptile, 3 days old"  
/lab\_host="DH10B"  
/clone\_lib="CH"



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RESULT 6
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LOCUS
DEFINITION CB858283 656 bp mRNA linear EST 22-APR-2003
3-PRIME, mRNA sequence.
ACCESSION CB858283
VERSION CB858283.1 GI:30052840
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 656)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 656 Std Error: 0.00
Plate: 6 row: H column: 4
Seq primer: T7.
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:555866"
/db_xref="taxon:112509"
/clone="HI06H04"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
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artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
ORIGIN
Query Match 11.3%; Score 544.2; DB 14; Length 656;
Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 667 CGCATCAGCGCTCTTCGCTTCCGCTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTG 726
DB 47 CGTATTGGCGCTCTTCGCTTCCGCTTCCGCTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTG 106
QY 727 CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
DB 107 CGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 166
QY 787 AACCGAGGAAAGAACTGTGAGCAAAAGCGCAAAAGCGCAAGGACCGTAAAGAGGC 846
DB 167 AACCGAGGAAAGAACTGTGAGCAAAAGCGCAAAAGCGCAAGGACCGTAAAGAGGC 226
QY 847 GCGTTCTCGCGCTTTTCCATAGGCTCCGCCCCCTCGAGAGCATCACAAAATCGACGC 906
DB 227 GCGTTCTCGCGCTTTTCCATAGGCTCCGCCCCCTCGAGAGCATCACAAAATCGACGC 286
QY 907 TCAAGTCAGAGGTGGCGAAACCGCAGGACTATAAGATACAGCGGTTTCCCTCTGA 966
DB 287 TCAAGTCAGAGGTGGCGAAACCGCAGGACTATAAGATACAGCGGTTTCCCTCTGA 346

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QY 967 AGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTCGCTTACCGGATACCTGTCCGCTTT 1026
DB 347 AGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTCGCTTACCGGATACCTGTCCGCTTT 406
QY 1027 CTCCTTCCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTG 1086
DB 407 CTCCTTCCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGGTG 466
QY 1087 TAGTGTGCTTCCGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCCAGCCCGACCGCTGC 1146
DB 467 TAGTGTGCTTCCGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTCCAGCCCGACCGCTGC 526
QY 1147 GCCTTATCCGCTAACTATCTGTGAGTCCAAACCCCGCTTAAGACACGACTTATCGCCACTG 1206
DB 527 GCCTTATCCGCTAACTATCTGTGAGTCCAAACCCCGCTTAAGACACGACTTATCGCCACTG 586
QY 1207 GCAGCAGCC 1215
DB 587 GCAGCAGCC 595

RESULT 7
BQ660152
LOCUS
DEFINITION BQ660152 669 bp mRNA linear EST 15-JUL-2002
3-PRIME, mRNA sequence.
ACCESSION BQ660152
VERSION BQ660152.1 GI:21801285
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 669)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 669 Std Error: 0.00
Plate: 1 row: D column: 8
Seq primer: T7.
FEATURES
Location/Qualifiers
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/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:1136544"
/db_xref="taxon:112509"
/clone="HI01D08"
/tissue_type="female inflorescences"
/dev_stage="female inflorescences (approx. 3 mm in size)"
/lab_host="XL10-Gold"
/clone_lib="HI"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
ORIGIN
Query Match 11.3%; Score 544.2; DB 13; Length 669;

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Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGCATCAGGCGCTTTCCTCGCTTCCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTCGCTG 726
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Db 67 CGTATTGGGCGCTTTCCTCGCTTCCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTG 126
  |||

QY 727 CGCGGAGCGGTATCAGTCTACTCANAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
  |||
Db 127 CGCGGAGCGGTATCAGTCTACTCANAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 186
  |||

QY 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 846
  |||
Db 187 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 246

QY 847 GCCTTCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGC 906
  |||
Db 247 GCCTTCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGC 306

QY 907 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCGCTGA 966
  |||
Db 307 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCGCTGA 366

QY 967 AGCTCCCTCGCTCGCTTCTCGTTCGAGACCTGCGGCTTACCGGATACCTGTCCGCGTTT 1026
  |||
Db 367 AGCTCCCTCGCTCGCTTCTCGTTCGAGACCTGCGGCTTACCGGATACCTGTCCGCGTTT 426

QY 1027 CTCCTTTCGGGAAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATCTCAGTTCCGGTG 1086
  |||
Db 427 CTCCTTTCGGGAAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATCTCAGTTCCGGTG 486

QY 1087 TAGGTCGTTCCGCTCAAGCTGGGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGC 1146
  |||
Db 487 TAGGTCGTTCCGCTCAAGCTGGGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGC 546

QY 1147 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 1206
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Db 547 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 606

QY 1207 GCAGCAGCC 1215
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Db 607 GCAGCAGCC 615
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RESULT 8
CB865829
LOCUS
DEFINITION CB865829 HD10N11w HD Hordeum vulgare cDNA clone HD10N11 3-PRIME, mRNA
sequence.
ACCESSION CB865829
VERSION CB865829.1 GI:30067805
KEYWORDS EST.
SOURCE
  ORGANISM Hordeum vulgare
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Poideae; Triticeae; Hordeum.
  1 (bases 1 to 677)
  Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
  EST sequencing and analysis in barley (2002)
  Unpublished (2002)
  JOURNAL
  COMMENT Contact: Stein Nils
  Molecular Markers Group, Department Genbank
  Institute of Plant Genetics and Crop Plant Research (IPK)
  Corrensstr. 3, 06466, Gatersleben, Germany
  Tel: 039482-5522
  Fax: 039482-5595
  Email: stein@ipk-gatersleben.de
  Insert Length: 677 Std Error: 0.00
  Plate: 10 row: N column: 11
  Seq primer: T7.
  Location/Qualifiers
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Query Match 11.3%; Score 544.2; DB 14; Length 677;
Best Local Similarity 99.5%; Pred. No. 7.8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGCATCAGGCGCTTTCCTCGCTTCCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTG 726
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Db 68 CGTATTGGGCGCTTTCCTCGCTTCCTCGCTCAGTCTCGCTCGCTCGCTCGCTCGCTG 127
  |||

QY 727 CGCGGAGCGGTATCAGTCTACTCANAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
  |||
Db 128 CGCGGAGCGGTATCAGTCTACTCANAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 187
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QY 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 846
  |||
Db 188 AACCGAGGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCCGTAAAGAGGCC 247
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QY 847 GCCTTCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGC 906
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Db 248 GCCTTCTGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCAAAAATCGACGC 307
  |||

QY 907 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCGCTGA 966
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Db 308 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCGCTGA 367
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QY 967 AGCTCCCTCGCTCGCTTCTCGTTCGAGACCTTACCGGATACCTGTCCGCGTTT 1026
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QY 1027 CTCCTTTCGGGAAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATCTCAGTTCCGGTG 1086
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Db 428 CTCCTTTCGGGAAAGCGTGGCGCTTTTCATAGTCAAGCTGTAGTATCTCAGTTCCGGTG 487
  |||

QY 1087 TAGGTCGTTCCGCTCAAGCTGGGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGC 1146
  |||
Db 488 TAGGTCGTTCCGCTCAAGCTGGGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGC 547
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QY 1147 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 1206
  |||
Db 548 GCCTTATCCGCTAACTATCTGTTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTG 607
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QY 1207 GCAGCAGCC 1215
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Db 608 GCAGCAGCC 616
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RESULT 9
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LOCUS
DEFINITION BQ660140 HI Hordeum vulgare subsp. vulgare cDNA clone HI01C11
3-PRIME, mRNA sequence.
ACCESSION BQ660140
VERSION BQ660140.1 GI:21801273
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727 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
Dbb 131 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 190
Qy 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGGCC 846
Dbb 191 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGGCC 250
Qy 847 GCGTGTGCGGTTTTCATAGCTCGCGCCCGCTGACGAGCATCAAAATTCAGCGC 906
Dbb 251 GCGTGTGCGGTTTTCATAGCTCGCGCCCGCTGACGAGCATCAAAATTCAGCGC 310
Qy 907 TCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACAGGGGTTTCCCGCTGGA 966
Dbb 311 TCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACAGGGGTTTCCCGCTGGA 370
Qy 967 AGCTCCCTCGTGGGCTCTCTGTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 1026
Dbb 371 AGCTCCCTCGTGGGCTCTCTGTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 430
Qy 1027 CTCCCTTCGGAGAGCGTGGGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTGGTG 1086
Dbb 431 CTCCCTTCGGAGAGCGTGGGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTGGTG 490
Qy 1087 TAGTGTGCTCGCTCCAGCTGGGCTGTGACAGAACCCCGCTTACCGCCGACCGCTGC 1146
Dbb 491 TAGTGTGCTCGCTCCAGCTGGGCTGTGACAGAACCCCGCTTACCGCCGACCGCTGC 550
Qy 1147 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCGCCACTG 1206
Dbb 551 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCGCCACTG 610
Qy 1207 GCAGCAGCC 1215
Dbb 611 GCAGCAGCC 619

RESULT 11
AJ281437
LOCUS
DEFINITION
4A3A-P4C3-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4C3, mRNA sequence.
ACCESSION
AJ281437
VERSION
AJ281437.1 GI:6929317
KEYWORDS
EST.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1. (bases 1 to 703)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B.
and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
Generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
PUBMED
10841561
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerhofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
1. 703
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4a r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4C3"
/cell_line="immune competent 4A3A"
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FEATURES
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Query Match 11.3%; Score 544.2; DB 9; Length 703;
Best Local Similarity 99.5%; Pred. No. 8e-114;
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 667 CGCATCAGGGCTCTCCGCTTCCTCGCTCACTGACTCGTGGCTCGGCTCGTTCGGCTG 726
Dbb 64 CGTATTGGGGCTCTCCGCTTCCTCGCTCACTGACTCGTGGCTCGGCTCGTTCGGCTG 123
Qy 727 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 786
Dbb 124 CGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGAT 183
Qy 787 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGGCC 846
Dbb 184 AACCGAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGAGGCC 243
Qy 847 GCGTGTGCGGTTTTCATAGCTCGCGCCCGCTGACGAGCATCAAAATTCAGCGC 906
Dbb 244 GCGTGTGCGGTTTTCATAGCTCGCGCCCGCTGACGAGCATCAAAATTCAGCGC 303
Qy 907 TCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACCGAGCGTTTCCCGCTGGA 966
Dbb 304 TCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACCGAGCGTTTCCCGCTGGA 363
Qy 967 AGCTCCCTCGTGGGCTCTCTGTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 1026
Dbb 364 AGCTCCCTCGTGGGCTCTCTGTTCCGACCGCTGCGGCTTACCGGATACCTGTCCGCGTTT 423
Qy 1027 CTCCCTTCGGAGAGCGTGGGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTGGTG 1086
Dbb 424 CTCCCTTCGGAGAGCGTGGGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTGGTG 483
Qy 1087 TAGTGTGCTCGCTCCAGCTGGGCTGTGACAGAACCCCGCTTACCGCCGACCGCTGC 1146
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Qy 1147 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCGCCACTG 1206
Dbb 544 GCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGGTGAAGACACGACTTATCGCCACTG 603
Qy 1207 GCAGCAGCC 1215
Dbb 604 GCAGCAGCC 612

RESULT 12
CF752100
LOCUS
DEFINITION
TGDR9 Human thyroid of Graves disease Subtractive Library Homo
sapiens cDNA, mRNA sequence.
ACCESSION
CF752100
VERSION
CF752100.1 GI:37659538
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 863)
Wen, G.-B., Wen, R. and Zhou, Y.
Screening and Cloning differentially expressed genes of Graves
disease by Suppression Subtractive Hybridization
Unpublished (2003)
JOURNAL
```



COMMENT

Contact: Ge-bo ,WEN  
Clinical Research Institute  
The First Hospital, Nanhua University  
The First Hospital, Nanhua University, Hengyang 421001, China  
Tel: 086-0734-8279196  
Fax: 086-0734-8279009  
Email: pikadious15@sohu.com  
The PCR primers binding area sequence have been removed .  
PCR Primers  
FORWARD: 5'-TCGAGCGCGCGCGCGCAGGT-3'  
BACKWARD: 5'-AGCGTGGTCGCGCGCAGGT-3'  
Insert Length: 320 Std Error: 0.00  
Seq primer: M13  
High quality sequence stop: 320  
POLYA=Yes.

FEATURES

source

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/strain="Chinese"  
/db\_xref="taxon:9606"  
/sex="female"  
/tissue\_type="Graves disease"  
/dev\_stage="Adult"  
/lab\_host="DH5a"  
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/notes="Organ: thyroid gland; Vector: pUCm-T; Site 1:  
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hybridization (SSH) to construct a subtractive library  
containing differentially expressed genes fragments  
between thyroid of Graves disease tissue and normal  
thyroid tissue, With PCR-Select #8482; cDNA Subtraction  
Kit( Clontech )."

ORIGIN

Query Match 11.3%; Score 544.2; DB 14; Length 863;  
Best Local Similarity 99.5%; Pred. No. 8.6e-114;  
Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 667 CGCATCAGGGCTTTCCGGTTCCTCGCTCAGTCTCGTGGCTCGGCTCGTTCGGCTG 726  
Db 90 CGTATTGGGGCTTTCCGGTTCCTCGCTCAGTCTCGTGGCTCGGCTCGTTCGGCTG 149

QY 727 CGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAGGGAT 786  
Db 150 CGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAGGGAT 209

QY 787 AACGCGAGAAAGAACATGTGAGCAAAAGCGCAAAAGCGCAAAAGCGCAAAAGCGCC 846  
Db 210 AACGCGAGAAAGAACATGTGAGCAAAAGCGCAAAAGCGCAAAAGCGCAAAAGCGCC 269

QY 847 GCGTTGCTGGCGTTTTTCCATAGGCTCGCGCCCTCGACGAGCATCACAAAATCGACGC 906  
Db 270 GCGTTGCTGGCGTTTTTCCATAGGCTCGCGCCCTCGACGAGCATCACAAAATCGACGC 329

QY 907 TCAAGTCAGAGTGGCGAAACCGACAGGACTATAAAGATACAGCGCTTTCCCGCTTGA 966  
Db 330 TCAAGTCAGAGTGGCGAAACCGACAGGACTATAAAGATACAGCGCTTTCCCGCTTGA 389

QY 967 AGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTCGCTTACCGGATACCTGTCGGCTTT 1026  
Db 390 AGCTCCCTCGTGGCTCTCCTGTTCCGACCCCTCGCTTACCGGATACCTGTCGGCTTT 449

QY 1027 CTCCTTCGGGAAGCTGGCGCTTTCTCATAGTCTACGCTGTAGGTATCTCAGTTCGGTG 1086  
Db 450 CTCCTTCGGGAAGCTGGCGCTTTCTCATAGTCTACGCTGTAGGTATCTCAGTTCGGTG 509

QY 1087 TAGGTCGTTCCGCTTCAAGCTGGGCTGTGTGACGAACCCCGCTTCAGCCCGACCGCTGC 1146  
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QY 1147 GCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACAGACTTATCGCCACTG 1206

Db 570 GCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACAGACTTATCGCCACTG 629

QY 1207 GCAGCAGCC 1215

Db 630 GCAGCAGCC 638

RESULT 13

BZ570738

LOCUS

DEFINITION

msh2\_1513.x1 msh Pseudomonas aeruginosa genomic clone msh2\_1513,  
genomic survey sequence.

ACCESSION

VERSION

BZ570738.1 GI:27205799

KEYWORDS

GSS.

SOURCE

ORGANISM

Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.

REFERENCE

1 (bases 1 to 966)

AUTHORS

Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
Burns,J.L., Kaul,R. and Olsen,M.V.

TITLE

Whole-Genome-Sequence variation among multiple isolates of  
Pseudomonas aeruginosa library

JOURNAL

J. Bacteriol. (2002) In press

COMMENT

Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.

FEATURES

Location/Qualifiers

1. .966  
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library."

ORIGIN

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Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 133 CGTATTGGGGCTTTCCGGTTCCTCGCTCAGTCTCGGCTCGGCTCGGCTCGGCTG 192

QY 727 CGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAGGGAT 786  
Db 193 CGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGGTTATCCACAGATCAGGGAT 252

QY 787 AACGCGAGAAAGAACATGTGAGCAAAAGCGCAAAAGCGCAAAAGCGCC 846  
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QY 847 GCGTTGCTGGCGTTTTTCCATAGGCTCGCGCCCTCGCTTACCGGATACCAAAAATCGACGC 906  
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QY 907 TCAAGTCAGAGTGGCGAAACCGACAGGACTATAAAGATACAGCGCTTTCCCGCTTGA 966  
Db 373 TCAAGTCAGAGTGGCGAAACCGACAGGACTATAAAGATACAGCGCTTTCCCGCTTGA 432

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QY 1207 GCAGCAGCC 1215
Db 673 GCAGCAGCC 681

RESULT 14
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DEFINITION ZMMBc0004E12f ZMMBc (EcoRI) Zea mays subsp. mays genomic clone
VERSION CG392995
KEYWORDS CG392995.1 GI:34336220
SOURCE GSS.
ORGANISM Zea mays subsp. mays (maize)
Ze mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1. (bases 1 to 996)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 11.
FEATURES
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Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 727 CGCGGAGCGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACAGAAATCAGGGAT 786
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Db 427 AACGCAGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCC 486
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Db 487 GGGTTGCTGGCGTGTTCATAGGTCCGCCCCCTCGAGAGATCACAATAATCGACGC 546
QY 907 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTTCCCGCTGGA 966
Db 547 TCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTTCCCGCTGGA 606
QY 967 AGTCCTCCTCGTGGCTCTCTGTTCCGACCTTCGCGTACCGGATACCTGTCGCTTT 1026
Db 607 AGTCCTCCTCGTGGCTCTCTGTTCCGACCTTCGCGTACCGGATACCTGTCGCTTT 666
QY 1027 CTCCTTCGGGAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTG 1086
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Db 727 TAGTTCGTTCCGCTCCAAAGCTGGGCTGTGTGTCAGCAACCCCGCTTCAGCCCGACCGCTGC 786
QY 1147 GCCTTATCCGGTAACCTATCGCTTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTG 1206
Db 787 GCCTTATCCGGTAACCTATCGCTTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTG 846
QY 1207 GCAGCAGCC 1215
Db 847 GCAGCAGCC 855

RESULT 15
LOCUS AU081124
DEFINITION AU081124 Oncorhynchus mykiss Kidney infected by infectious
hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KG'12,
mRNA sequence.
ACCESSION AU081124
VERSION AU081124.1 GI:6431472
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1. (bases 1 to 1089)
Kono,T., Sakai,M. and Lapetra,S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakukenbikanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES
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hematopoietic necrosis virus"

ORIGIN
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Matches 546; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy	727	CGGGAGCGGTATCAGTCTCACTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGAT	786
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Qy	787	AACGACGAAAGAACATGTGAGCAAAAGGCGCAGCAAGGCCAGGAAACCGTAAAGGCC	846
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Qy	847	GCCTTGTGCGGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGC	906
Db	486	GCCTTGTGCGGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGC	545
Qy	907	TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTCCGCTTGA	966
Db	546	TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACAGGGGTTTCCGCTTGA	605
Qy	967	AGCTCCCTCGTGGCTCTCTCTTTCGACCGCTTACCGGATACCTGTCCGCTTT	1026
Db	606	AGCTCCCTCGTGGCTCTCTCTTTCGACCGCTTACCGGATACCTGTCCGCTTT	665
Qy	1027	CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG	1086
Db	666	CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG	725
Qy	1087	TAGGTGCTTCGCTCCAGCTGGGCTGTGTGCAGAACCCCGCTTACGCCGACCGCTGC	1146
Db	726	TAGGTGCTTCGCTCCAGCTGGGCTGTGTGCAGAACCCCGCTTACGCCGACCGCTGC	785
Qy	1147	GCCTTATCCGTAACATATCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCACCTG	1206
Db	786	GCCTTATCCGTAACATATCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCACCTG	845
Qy	1207	GCAGCAGCC	1215
Db	846	GCAGCAGCC	854

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